

FIG.1A.

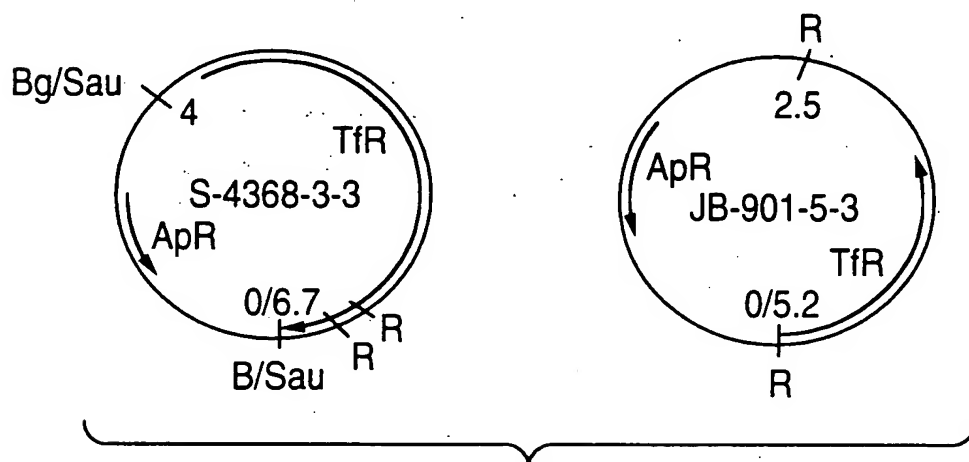


FIG.1B.

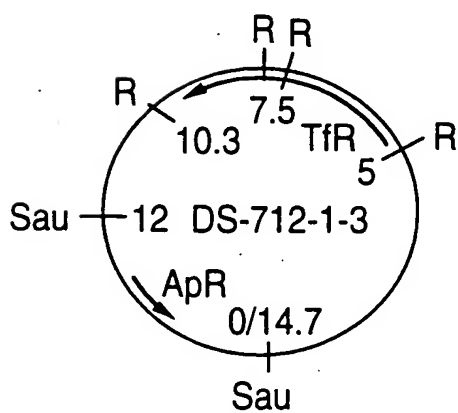


FIG.1C.

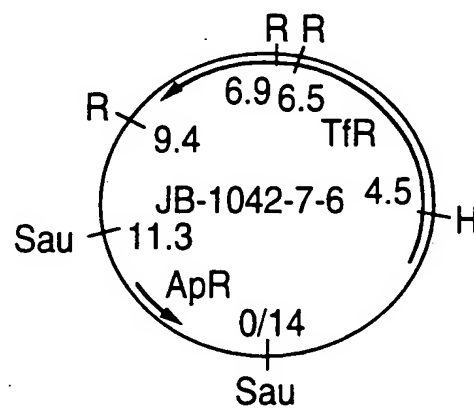


FIG.1D.

FIG. 3 A.

TATAACTCA ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe
 1 5 10

 TTA CTA AGT GCT TGT AGC GGA GGG GGG TCT TTT GAT GTA CAT AAC GTC
Leu Leu Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val
 15 20 25

 TCT AAT ACC CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT TCA AGT
 Ser Asn Thr Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser
 30 35 40 45

 TCA AGA ACA AAA TCT AAA TTG GAA AAG TTG TCC ATT CCT TCT TTA GGG
 Ser Arg Thr Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly
 50 55 60

 GGA GGG ATG AAG TTA GCG GCT CTG AAT CTT TTT GAT AGG A-C AAA CCT
 Gly Gly Met Lys Leu Ala Ala Leu Asn Leu Phe Asp Arg Asn Lys Pro
 65 70 75

 AGT CTC TTA AAT GAA GAT AGC TAT ATG ATA TTT TCC TCA CGT TCT ACG
 Ser Leu Leu Asn Glu Asp Ser Tyr Met Ile Phe Ser Ser Arg Ser Thr
 80 85 90

ATT GAA GAG GAT GTT AAA AAT GAC AAT CAA AAC GGC GAG CAC CCT ATT
Ile Glu Glu Asp Val Lys Asn Asp Asn Gln Asn Gly Glu His Pro Ile
95 . 100 105

GAC TCA ATA GTC GAT CCT AGA GCA CCA AAT TCA AAC GAA AAT CGT CAT
Asp Ser Ile Val Asp Pro Arg Ala Pro Asn Ser Asn Glu Asn Arg His
110 115 120 125

CGA CAA AAA TAT GTA TAT TCA GGG CTT TAT TAT ATT CAA TCG TGG AGT
Gly Gln Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser
130 135 140

CTA AGA GAT TTA CCA AAT AAA AAG TTT TAT TCA GGT TAC TAT GGA TAT
Leu Arg Asp Leu Pro Asn Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr Tyr
145 150 155

GGG TAT TAC TTT GGC AAT ACA ACT GCC TCT GCA TTA CCT GTA GGT GGC
Ala Tyr Tyr Phe Gly Asn Thr Thr Ala Ser Ala Leu Pro Val Gly Gly
160 165 170

GTA GCA ACG TAT AAA GGA ACT TGG AGC TTC ACC GCA GCT GAA AAT
 Val Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn
 175 180 185

FIG.3C.

GGC AAG AAT TAT GAA TTG TTA AGA AAT TCT GGT GGC GGT CAA GCT TAT
 Gly Lys Asn Tyr Glu Leu Leu Arg Asn Ser Gly Gly Gln Ala Tyr
 190 195 200 205

TCT CGA CGT AGT GCT ACT CCA GAA GAT ATT GAT TTA GAT CGT AAG ACG
 Ser Arg Arg Ser Ala Thr Pro Glu Asp Ile Asp Leu Asp Arg Lys Thr
 210 215 220

GGC TTA ACA AGT GAA TTT ACT GTC AAT TTT GGT ACA AAA AAG CTC ACT
 Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr
 225 230 235

CGA CGA CTT TAT TAT AAT TTA CGT GAA ACA GAT GCT AAT AAA TCA CAA
 Gly Gly Leu Tyr Tyr Asn Leu Arg Glu Thr Asp Ala Asn Lys Ser Gln
 240 245 250

AAT AGA ACA CAT AAA CTC TAC GAT CTA GAA GCT GAT GTT CAT AGC AAC
 Asn Arg Thr His Lys Lys Leu Tyr Asp Leu Glu Ala Asp Val His Ser Asn
 255 260 265

CGA TTC AGG GGT AAA GTA AAG CCA ACC AAA AAG GAG TCT TCT GAA GAA
 Arg Phe Arg Gly Lys Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu
 270 275 280 285

FIG.3D.

CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAC GGG CCT
His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro
290 295 300

GAG GGT CAA GAA TTA GGA GGA AAG TTT TTA GCT CAC GAC AAA AAA GTT
Glu Gly Gln Glu Leu Gly Gly Lys Phe Leu Ala His Asp Lys Lys Val
305 310 315

TTG GGG GTA TTT AGT GCC AAA GAA CAG CAA GAA ACG TCA GAA AAC AAA
Leu Gly Val Phe Ser Ala Lys Glu Gln Gln Glu Thr Ser Glu Asn Lys
320 325 330

AAA TTA CCC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTT AAA
Lys Leu Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Lys
335 340 345

ACA ACC AAT GCA ACA GCC AAT GCA ACA ACC GAT GCA ACA ACC AGT ACA
Thr Thr Asn Ala Thr Ala Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr
350 355 360 365

ACA GCC AGT ACA AAA ACC GAT ACA ACA ACC AAT GCA ACA GCC AAT ACA
Thr Ala Ser Thr Lys Thr Asp Thr Thr Thr Asn Ala Thr Ala Asn Thr
370 375 380

FIG. 3E.

GAA AAC TTT ACG ACA AAA GAT ATA CCA AGT TTG GGT GAA GCT GAT TAT
Glu Asn Phe Thr Thr Lys Asp Ile Pro Ser Leu Gly Glu Ala Asp Tyr
385 390 395

CIT TTA ATT GAT AAT TAC OCT CTT GTT CCT CTT TTC OCT GAG AGT GGT GAT
Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Phe Pro Glu Ser Gly Asp
400 405 410

TTC ATA AGT AGT AAG CAC CAT ACT GTA GGA AAG AAA ACC TAT CAA GTA
Phe Ile Ser Ser Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val
415 420 425

GAA GCA TGT TGC AGT AAT CTA AGC TAT GTA AAA TTT GGT ATG TAT TAT
Glu Ala Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr
430 435 440 445

GAA GCC CCA CCT AAA GAA GAA GAA AAA GAA AAA GAA AAA GAC AAA GAC
Glu Ala Pro Pro Lys Glu Glu Glu Lys Glu Lys Glu Lys Asp Lys Asp
450 455 460

AAA GAA AAA GAA AAA CAA GCG ACA ACA TCT ATC AAG ACT TAT TAT CAA
Lys Glu Lys Glu Lys Gln Ala Thr Thr Ser Ile Lys Thr Tyr Tyr Gln
465 470 475

FIG. 3F.

TTC TTA TTA GGT CTC CGT ACT CCC AGT TCT GAA ATA CCT AAA GAA GGA
Phe Leu Leu Gly Leu Arg Thr Pro Ser Ser Glu Ile Pro Lys Glu Gly
480 485 490

AGT GCA AAA TAT CAT GGT AAT TGG TTT GGT TAT ATT AGT GAT GGC GAG
Ser Ala Lys Tyr His Gly Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu
495 500 505

ACA TCT TAC TCC GCC AGT GGT GAT AAG GAA CGC AGT AAA AAT GCT GTC
Thr Ser Tyr Ser Ala Ser Gly Asp Lys Glu Arg Ser Lys Asn Ala Val
510 515 520 525

GCC GAG TTT AAT GTA AAT TTT GCC GAG AAA ACA TTA ACA GGC GAA TTA
Ala Glu Phe Asn Val Asn Phe Ala Glu Lys Thr Leu Thr Gly Glu Leu
530 535 540

AAA CGA CAC GAT ACT CAA AAT CCC GTA TTT AAA ATT AAT GCA ACC TTT
Lys Arg His Asp Thr Gln Asn Pro Val Phe Lys Ile Asn Ala Thr Phe
545 550 555

CAA AGT GGT AAG AAT GAC TTC ACT GGT ACA GCA ACC GCA AAA GAT TTA
Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Lys Asp Leu
560 565 570

FIG. 36.

GCA ATA GAT GGT AAA AAT ACA CAA GGC ACA TCT AAA GTC AAT TTC ACG
Ala Ile Asp Gly Lys Asn Thr Gln Gly Thr Ser Lys Val Asn Phe Thr
575 580

GCA ACA GTA AAC GGG GCA TTT TAT GGT CCG CAC GCT ACA GAA TTA GGC
Ala Thr Val Asn Gly Ala Phe Tyr Gly Pro His Ala Thr Glu Leu Gly
590 600 605

GGT TAT TTC ACC TAT AAC GGA AAC AAT CCT ACA GAT AAA AAT TCA TCA
Gly Tyr Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser Ser
610 620

TCC AAT TCA GAA AAG GCA AGA GCT GCC GTT GTG TTT GGA GCT AAA AAA
Ser Asn Ser Glu Lys Ala Arg Ala Val Val Phe Gly Ala Lys Lys
625 630 635

CAA CAA GTA GAA ACA ACC AA GTAATGGAAT ACTAAA A ATG ACT AAA AAA
Gln Gln Val Glu Thr Thr Lys Met Thr Lys Lys
640 645

CCC TAT TTT CGC CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT
Pro Tyr Phe Arg Leu Ser Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr
650 655 660

FIG. 3H.

GTA AAA GCA GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA
 Val Lys Ala Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser
 665 670 680
 TCT GAA GTG GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC
 Ser Glu Val Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile
 685 690 695
 TCA GTC ACT GCA GAA AAA GTT AGA GAT CGT AAA GAT AAT GAA GTA ACT
 Ser Val Thr Ala Glu Lys Val Arg Asp Arg Lys Asp Asn Glu Val Thr
 700 705 710
 GGA CTT GGC AAA ATT ATA AAA ACT AGT GAA AGT ATC AGC CGA GAA CAA
 Gly Leu Gly Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln
 715 720 725
 GTA TTA AAT ATT CGT GAT CTA ACA CGC TAT GAT CCA GCG ATT TCA GTT
 Val Leu Asn Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val
 730 735 740
 GTA GAA CAA GGT CGC GGT GCA AGT TCT GCA TAT TCT ATT CGT GGT ATG
 Val Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met
 745 750 755 760

FIG.31.

GAC AGA AAT AGA GTT GCT TTA GTA GAT GGT TTA CCT CAA ACG CAA
Asp Arg Asn Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln 775
765 770

TCT TAT GTA GTG CAA AGC CCT TTA GTT GCT CGT TCA GGA TAT TCT GGC
Ser Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly 790
780 785

ACT CGT GCA ATT AAT GAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA
Thr Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu 805
795 800

ATA AGC AAG GGG GGG AGT TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT
Ile Ser Lys Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala 820
810 815

GGT TCT GTA ACA TTT CAA AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA
Gly Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly 840
825 830 835

GAC AAA TCA TGG GGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT
Asp Lys Ser Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn 855
845 850

FIG. 3J.

AAA GGC TTT ACC CAT TCT TTA CCT GTA GCA AAA CAA GGT GGA TTT
Lys Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe
860 865 870

GAA GGG GTC GCC ATT TAC ACT CAC CGA AAT TCA ATT GAA ACC CAA GTC
Glu Gly Val Ala Ile Tyr Thr His Arg Asn Ser Ile Glu Thr Gln Val
875 880 885

CAT AAA GAT GCA TTA AAA GGC GTG CAA AGT TAT GAT CGA TTC ATC GCC
His Lys Asp Ala Leu Lys Gly Val Gln Ser Tyr Asp Arg Phe Ile Ala
890 895 900

ACA ACA GAG GAT CAA TCT GCA TAC TTT GTG ATG CAA GAT GAG TGT CTA
Thr Thr Glu Asp Gln Ser Ala Tyr Phe Val Met Gln Asp Glu Cys Leu
905 910 915 920

GAT CGT TAT GAC AAG TGT AAA ACT TCA CCC AAA CGA CCT GCG ACT TTA
Asp Gly Tyr Asp Lys Cys Lys Thr Ser Pro Lys Arg Pro Ala Thr Leu
925 930 935

TCC ACC CAA AGA GAA ACC GTA AGC GTT TCA GAT TAT ACG GGG GCT AAC
Ser Thr Gln Arg Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn
940 945 950

FIG.3K.

CGT ATC AAA CCT AAT CCA AUG AAA TAT GAA AGC CAG TCT TGG TTT TTA
Arg Ile Lys Pro Asn Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu
955 960 965

AGA GGA GGT TAT CAT TTT TCT GAA CAA CAC TAT ATT GGT GGT ATT TTT
Arg Gly Gly Tyr His Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe
970 975 980

GAA TTC ACA CAA CAA AAA TTT GAT ATC CGT GAT AUG ACA TTT CCC GGT
Glu Phe Thr Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala
985 990 995 1000

TAT TTA AGG CCA ACA GAA GAC AAG GAT TTA CAA AGT CGC CCT TTT TAT
Tyr Leu Arg Pro Thr Glu Asp Lys Asp Leu Gln Ser Arg Pro Phe Tyr
1005 1010 1015

CCA AAG CAA GAT TAT GGT GCA TAT CAA CAT ATT GGT GAT GGC AGA GGC
Pro Lys Gln Asp Tyr Gly Ala Tyr Gln His Ile Gly Asp Gly Arg Gly
1020 1025 1030

GTT AAA TAT GCA AGT GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG
Val Lys Tyr Ala Ser Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln
1035 1040 1045

FIG.3L.

CGT GTA GGT ATT GAA TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC
Arg Val Gly Ile Glu Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile
1050 1055 1060

ATT GAC AAA GCG GIG TTA AGT GCT AAT CAA ACA TCA TAC TTG ACA
Ile Asp Lys Ala Val Leu Ser Ala Asn Gln Thr Ser Tyr Leu Thr
1065 1070 1075 1080

GTT ATA TGC GAC ATA CGC ATT GCA GTC TTT ATC CAT AAT CCA AGT AAG
Val Ile Cys Asp Ile Arg Ile Ala Val Phe Ile His Asn Pro Ser Lys
1085 1090 1095

AAT TGC CGC CCA ACA CTT GAT AAA CCT TAT TCA TAC TAT CAT TCT GAT
Asn Cys Arg Pro Thr Leu Asp Lys Pro Tyr Ser Tyr Tyr His Ser Asp
1100 1105 1110

AGA AAT GTT TAT AAA GAA AAA CAT AAC ATG TTG CAA TTG AAT TTA GAG
Arg Asn Val Tyr Lys Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu
1115 1120 1125

AAA AAA ATT CAA CAA AAT TGG CTT ACT CAT CAA ATT GCC TTC AAT CTT
Lys Lys Ile Gln Gln Asn Trp Leu Thr His Gln Ile Ala Phe Asn Leu
1130 1135 1140

FIG. 3M.

GGT TTT GAT GAC TTT ACT TCC GCA CTT CAG CAT AAA GAT TAT TTA ACT
Gly Phe Asp Asp Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr
1145 1150 1155 1160

CGA CGT GTT ATC GCT ACG GCA AGT AGT ATT TCA GAG AAA CGT GGT GAA
Arg Arg Val Ile Ala Thr Ala Ser Ser Ile Ser Glu Lys Arg Gly Glu
1165 1170 1175

GCA AGA AGA AAT GGT TTA CAA TCA AGT CCT TAC TTA TAC CCA ACA CCA
Ala Arg Arg Asn Gly Leu Gln Ser Ser Pro Tyr Leu Tyr Pro Thr Pro
1180 1185 1190

AAA GCA GAG TTG GTA GCA GCA GAT CTT TGT AAT TAT CAA GGT AAG TCC
Lys Ala Glu Leu Val Gly Gly Asp Leu Cys Asn Tyr Gln Gly Lys Ser
1195 1200 1205

TCT AAT TAC AGT GAC TGT AAA GTG CCG TTA ATT AAA GGG AAA AAT TAT
Ser Asn Tyr Ser Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr
1210 1215 1220

TAT TTC GCA GCA CGC AAT AAT ATG GCA TTA GCG AAA TAC GTT GAT TTA
Tyr Phe Ala Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Val Asp Leu
1225 1230 1235 1240

FIG. 3N.

GGT TTA GGT ATG AGG TAT GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA
Gly Leu Gly Met Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser
1245 1250 1255

ACT ATT AGT GTT GGT AAA TTT AAA AAT TTC TCT TGG AAT ACT GGT ATT
Thr Ile Ser Val Gly Lys Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile
1260 1265 1270

GTC ATA AAA CCA ACG GAA TGG CTT GAT CTT TCT TAT CGC CTT TCT ACT
Val Ile Lys Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr
1275 1280 1285

CGA TTT AGA AAT CCT AGT TTT GCT GAA ATG TAT GGT TGG CCG TAT GGT
Gly Phe Arg Asn Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Tyr Gly
1290 1295 1300

GGC AAG GAT ACC GAT GTT TAT ATA GGT AAA TTT AAG CCT GAA ACA TCT
Gly Lys Asp Thr Asp Val Tyr Ile Gly Lys Phe Lys Pro Glu Thr Ser
1305 1310 1315 1320

CGT AAC CAA GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT
Arg Asn Gln Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile
1325 1330 1335

FIG.30.

GAG ATC AGT CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT
Glu Ile Ser His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala
1340 1345 1350

GAA GAA CTT AGT AAA AAT GGA ACT ACT GGA AAG GGC AAT TAT GGA TAT
Glu Glu Leu Ser Lys Asn Gly Thr Thr Gly Lys Gly Asn Tyr Gly Tyr
1355 1360 1365

CAT AAT GCA CAA AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCG CAA
His Asn Ala Gln Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln
1370 1375 1380

TTA GAT TTT AAT GGT TTA TGG AAA CGT ATT CCC TAC GGT TGG TAT GCA
Leu Asp Phe Asn Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala
1385 1390 1395 1400

ACA TTT GCT TAT AAC CGA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT
Thr Phe Ala Tyr Asn Arg Val Lys Val Lys Asp Gln Lys Ile Asn Ala
1405 1410 1415

GGT TTA GCT TCC GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC
Gly Leu Ala Ser Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser
1420 1425 1430

FIG.3P.

CGT TAT ATC ATT GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG CGA
Arg Tyr Ile Ile Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly
1435 1440 1445

ATT AAG ACA ATG TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG
Ile Lys Thr Met Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu
1450 1455 1460

CTA GGA AAA CGT GCA TTG GGT AAC AAT TCA AGG AAT GTA AAA TCA ACA
Leu Gly Lys Arg Ala Leu Gly Asn Asn Ser Arg Asn Val Lys Ser Thr
1465 1470 1475 1480

AGA AAA CTT ACT CGG GCA TGG CAT ATC TTA GAT GTA TCG GGT TAT TAC
Arg Lys Leu Thr Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr
1485 1490 1495

ATG GTG AAT AGA AGT ATT TTG TTC CGA TTA GGA GTA TAT AAT TTA TTA
Met Val Asn Arg Ser Ile Leu Phe Arg Leu Gly Val Tyr Asn Leu Leu
1500 1505 1510

AAC TAT CGC TAT GTC ACT TGG GAA GCG GTG CGT CAA ACA GCA CAA GGT
Asn Tyr Arg Tyr Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly
1515 1520 1525

FIG.3Q.

GCG GTC AAT CAA CAT CAA AAT GTT GGT AAC TAT ACT CGC TAC GCA GCA	
Ala Val Asn Gln His Gln Asn Val Gly Asn Tyr Thr Arg Tyr Ala Ala	
1530	1535
	1540
TCA GCA CGA AAC TAT ACC TTA ACA TTA GAA ATG AAA TTC TAA	
Ser Gly Arg Asn Tyr Thr Leu Thr Leu Glu Met Lys Phe	
1545	1550
	1555

FIG. 4 A.

GCCCAAGCTA CATIGGTTAA TGATAAGCCT ATAAATGATA AGAAGAAAT TIGTTTTACG

CCATTTTICA TATTTTATCC ATGAACITAA AAAACTCTAA CTIGACATTA TTACAAAAAA
-35

AGATCAATAA TGGCAATTAT TATCAATTTT GATGAGTAT ATAATTCT ATG AAA TCT
-10 RBS
Met Lys Ser
1

GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT GCT TGT AGC
Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser Ala Cys Ser
5 10 15

GGA GGG GGG TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC CCC TCT TCT
Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr Pro Ser Ser
20 25 30 35

AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA AAA AAA TCT AAT
Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys Lys Ser Asn
40 45 50

TTG AAA AAG TTG TTC ATT OCT TCT TTA GGA GGA GGG ATG AAA TTG GTG
Leu Lys Lys Leu Phe Ile Pro Ser Leu Gly Gly Gly Met Lys Leu Val
55 60 65

FIG. 4B.

GCT CAG AAT CTT CGT GGT AAT AAA GAA CCT AGT TTC TTA AAT GAA GAT
Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu Asn Glu Asp
70 75 80

GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ACG ATT GAA AAG GAT GTT
Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu Lys Asp Val
85 90 95

AAA GAT AAC AAT AAA AAC GGG GCG GAC CTT ATT GGC TCA ATA GAC GAG
Lys Asp Asn Asn Lys Asn Gly Ala Asp Leu Ile Gly Ser Ile Asp Glu
100 105 110 115

CCT AGT ACA ACA AAT CCA CCC GAA AAG CAT CAT GGA CAA AAA TAT GTA
Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln Lys Tyr Val
120 125 130

TAT TCA GGG CTT TAT TAT ACT CCA TCG TGG AGT TTA AAC GAT TCT AAA
Tyr Ser Gly Leu Tyr Tyr Thr Pro Ser Ser Trp Ser Leu Asn Asp Ser Lys
135 140 145

AAC AAG TTT TAT TTA GGT TAC TAT GGA TAT CCG TTT TAT TAT GGT AAT
Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr Gly Asn
150 155 160

FIG.4C.

AAA ACT GCA ACA AAC TTG CCA GTA AAC GGT GTA GCT AAA TAC AAA GGA
Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys Tyr Lys Gly
165 170 175

ACT TGG GAT TTC ATC ACT GCA ACT AAA AAT GGC AAA CGT TAT CCT TTG
Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg Tyr Pro Leu
180 185 190 195

TTA AGT AAT GGC AGT CAC GCT TAT TAT CGA CGT AGT GCA ATT CCA GAA
Leu Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala Ile Pro Glu
200 205 210

GAT ATT GAT TTA GAA AAT GAT TCA AAG AAT GGT GAT ATA GGC TTA ATA
Asp Ile Asp Leu Glu Asn Asp Ser Lys Asn Gly Asp Ile Gly Leu Ile
215 220 225

AGT GAA TTT AGT GCA GAT TTT GGG ACT AAA AAA CTG ACA GGA CAA CTG
Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr Gly Gln Leu
230 235 240

TCT TAC ACC AAA AGA AAA ACT AAT AAT CAA CCA TAT GAA AAG AAA AAA
Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu Lys Lys Lys
245 250 255

FIG.4D.

CTC TAT GAT ATA GAT GCC GAT ATT TAT AGT AAT AGA TTC AGG GGT ACA
Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe Arg Gly Thr
260 265 270 275

GTA AAG CCA ACC GAA AAA GAT TCT GAA GAA CAT CCC TTT ACC AGC GAG
Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe Thr Ser Glu
280 285 290

CGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA GAA CTA GGG
Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly
295 300 305

GGG AAA TTT TTA GCT ACG GAT AAC CGA GGT TTT GGG GTA TTT AGT GCC
Gly Lys Phe Leu Ala Thr Asp Asn Arg Val Phe Gly Val Phe Ser Ala
310 315 320

AAA GAA ACG GAA GAA ACA AAA AAG GAA GCG TTA TCC AAG GAA ACC TTA
Lys Glu Thr Glu Glu Thr Lys Lys Glu Ala Leu Ser Lys Glu Thr Leu
325 330 335

ATT GAT GGC AAG CTA ATT ACT TTC TCT ACT AAA AAA ACC GAT GCA AAA
Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr Asp Ala Lys
340 345 350 355

FIG.4E.

ACC AAT GCA ACA ACC AGT ACC GCA GCT AAT ACA ACA ACC GAT ACA ACC
 Thr Asn Ala Thr Thr Ser Thr Ala Ala Asn Thr Thr Thr Asp Thr Thr
 360 365 370

GCC AAT ACA ATA ACC GAT GAA AAA AAC TTT AAG ACG GAA GAT ATA TCA
 Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu Asp Ile Ser
 375 380 385

AGT TTT GGT GAA GCT GAT TAT CTG TTA ATT GAC AAA TAT CCT ATT CCA
 Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Lys Tyr Pro Ile Pro
 390 395 400

CIT TTA CCT GAT AAA AAT ACT AAT GAT TTC ATA AGT AGT AAG CAT CAT
 Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser Lys His His
 405 410 415

ACT GTA GGA AAT AAA CGC TAT AAA GTG GAA GCA TGT TGC AGT AAT CTA
 Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Cys Ser Asn Leu
 420 425 430 435

AGC TAT GTG AAA TTT GGT ATG TAT TAT GAA GAC CCA CTT AAA GAA AAA
 Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu Lys Glu Lys
 440 445 450

FIG.4F.

GAA ACA GAA ACA GAA ACA GAA ACA GAA AAA GAA AAA GAA AAA
Glu Thr Glu Thr Glu Thr Glu Thr Lys Asp Lys Glu Lys Glu Lys 455 460 465

GAA AAA GAC AAA GAC AAA GAA AAA CAA ACG GCG GCA ACG ACC AAC ACT
Glu Lys Asp Lys Asp Lys Glu Lys Gln Thr Ala Ala Thr Thr Asn Thr 470 475 480

TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT CCC AAG GAC GAC ATA CCT
Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Lys Asp Asp Ile Pro 485 490 495

AAA ACA GGA AGT GCA AAA TAT CAT GGT AGT TGG TTT GGT TAT ATT ACT
Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Trp Phe Gly Tyr Ile Thr 500 505 510 515

GAC GGT AAG ACA TCT TAC TCC CCC AGT GGT GAT AAG AAA CGC GAT AAA
Asp Gly Lys Thr Ser Tyr Ser Pro Ser Gly Asp Lys Lys Arg Asp Lys 520 525 530

AAT GCT GTC GCC GAG TTT AAT GTT GAT TTT GCC GAG AAA AAG CTA ACA
Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys Lys Leu Thr 535 540 545

FIG.4G.

GCG GAA TTA AAA CGA CAC GAT ACT GGA AAT CCC GTA TTT AGT ATT GAG
Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe Ser Ile Glu
550 555 560

GCA AAC TTT AAT AAT AGT AGT AAT GGC TTC ACT GGT ACA GCA ACC GCA
Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr Ala Thr Ala
565 570 575

ACA AAT TTT GTA ATA GAT GGT AAA AAT AGT CAA AAT AAA AAT ACC CCA
Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys Asn Thr Pro
580 585 590 595

ATT AAT ATT ACA ACT AAA GTA AAC GGG GCA TTT TAT GGA CCT AAG GCT
Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly Pro Lys Ala
600 605 610

TCT GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAT TCT ACA GCT ACA
Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Ser Thr Ala Thr
615 620 625

AAT TCT GAA AGT TCC TCA ACC GTA TCT TCA TCC AAT TCA AAA AAT
Asn Ser Glu Ser Ser Thr Val Ser Ser Ser Asn Ser Lys Asn
630 635 640

FIG.4H.

GCA AGA GCT GCA GTT GTC TTT GGT GCG AGA CAA CAA GTA GAA ACA ACC
 645 650
 Ala Arg Ala Ala Val Val Phe Gly Ala Arg Gln Val Glu Thr Thr

AAA TAATCGAATA CTAAAA ATG ACT AAA AAA CCC TAT TTT CGC CTA AGT
 Lys Met Thr Lys Lys Pro Tyr Phe Arg Leu Ser
 660 665 670

ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT GTA AAA GCA GAA ACT CAA
 675 680 685
 Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr Val Lys Ala Glu Thr Gln

AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG GAC ACT CAA
 690 695 700
 Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser Glu Val Asp Thr Gln

AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT GCA GAA AAA
 705 710 715
 Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser Val Thr Ala Glu Lys

ATA AGA GAT CGT AAA GAT AAT GAA GTA ACT GCA CTT GGC AAA ATT ATC
 720 725 730
 Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly Leu Gly Lys Ile Ile

ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA AGC AAG GGG GGG AGT
Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Gly Ser 830
815 820 825

FIG.4J.

TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT GGT TCT GTA ACA TTT CAA
 Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Thr Phe Gln
 835 840 845

AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA TGG GGA ATT
 Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser Trp Gly Ile
 850 855 860

CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT ACC CAT TCT
 Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe Thr His Ser
 865 870 875

TTA GCT GTA GCA GGA AAA CAA GGT GGA TTT GAA GCG CTA GCC ATT TAC
 Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu Gly Leu Ala Ile Tyr
 880 885 890

ACT CAA CGA AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT GCA TTA AAA
 Thr Gln Arg Asn Ser Ile Glu Thr Gln Val His Lys Asp Ala Leu Lys
 895 900 905 910

GGC GTA CAA AGT TAT GAT CGA TTA ATC GCC ACA ACA GAT AAA TCT TCA
 Gly Val Gln Ser Tyr Asp Arg Leu Ile Ala Thr Thr Asp Lys Ser Ser
 915 920 925

FIG.4K.

GGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT GGT GAT GAC AAG TGT
 Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn Gly Asp Asp Lys Cys
 930 935 940

GCA GCC AAG CCA CCT GCG ACT TTA TCC ACC CAA AGC GAA ACC GTA AGC
 Ala Ala Lys Pro Pro Ala Thr Leu Ser Thr Gln Ser Glu Thr Val Ser
 945 950 955

GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA CCT AAT CCA ATG AAA
 Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn Pro Met Lys
 960 965 970

TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GGG TAT CAT TTT TCT GAA
 Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Gly Tyr His Phe Ser Glu
 975 980 985 990

CAA CAT TAT ATT GGT GGT ATT TTT GAA TTC ACA CAA CAA AAA TTT GAT
 Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln Lys Phe Asp
 995 1000 1005

ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGC CCA ACA GAA AGA CCG
 Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Ser Pro Thr Glu Arg Arg
 1010 1015 1020

FIG. 4L.

GAT GAT AGT AGT CGT TCT TTT TAT CCA ATG CAA GAT CAT GGT GCA TAT
 Asp Asp Ser Ser Arg Ser Phe Tyr Pro Met Gln Asp His Gly Ala Tyr
 1025 1030 1035

CAA CAT ATT GAG GAT GGC AGA GGC GTT AAA TAT GCA AGT GGG CTT TAT
 Gln His Ile Glu Asp Gly Arg Gly Val Lys Tyr Ala Ser Gly Leu Tyr
 1040 1045 1050

TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT ATT GAA TAT ATT TAC
 Phe Asp Glu His His Arg Lys Lys Gln Arg Val Gly Ile Glu Tyr Ile Tyr
 1055 1060 1065 1070

GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA GCA GIG TTA AGT GCT
 Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val Leu Ser Ala
 1075 1080 1085

AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG CCA CAT ACG CAT TGC
 Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Arg His Thr His Cys
 1090 1095 1100

AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA CTT GAT AAA
 Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr Leu Asp Lys
 1105 1110 1115

FIG. 4M.

CCT TAT TCA TAC TAT CGT TCT GAT AGA AAT GTT TAT AAA GAA AAA CAT	
Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val Tyr Lys Glu Lys His	
1120	1125
	1130
AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA AAT CAA CAA AAT TCG CTT	
Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln Asn Trp Leu	
1135	1140
	1145
	1150
ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT GAC TTT ACT TCA GCG	
Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe Thr Ser Ala	
1155	1160
	1165
CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ATC GCT ACG GCA GAT	
Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Ile Ala Thr Ala Asp	
1170	1175
	1180
AGT ATT CCA AGG AAA CCT GGT GAA ACT GGT AAA CCA AGA AAT GGT TTG	
Ser Ile Pro Arg Lys Pro Gly Glu Thr Gly Lys Pro Arg Asn Gly Leu	
1185	1190
	1195
CAA TCA CAA CCT TAC TTA TAC CCA AAA CCA GAG CCA TAT TTT GCA GGA	
Gln Ser Gln Pro Tyr Leu Tyr Pro Lys Pro Glu Pro Tyr Phe Ala Gly	
1200	1205
	1210

TTGG CTT GAT CTT TCT TAT CGC CTT TCT ACT GGA TTT AGA AAT CCT AGT
 1295
 TTrp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg Asn Pro Ser
 1300 1305 1310

FIG.40.

TTT TCT GAA ATG TAT GGT TGG CGG TAT GGT GGC AAG AAT GAC GAG GTT
 Phe Ser Glu Met Tyr Gly Trp Arg Tyr Gly Gly Lys Asn Asp Glu Val
 1315 1320 1325

 TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA GAG TTT GGT
 Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln Glu Phe Gly
 1330 1335 1340

 CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT CAT TTT AGT
 Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser His Phe Ser
 1345 1350 1355

 AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT AGT AAA AAT
 Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu Ser Lys Asn
 1360 1365 1370

 CGA ACT CGA AAG GGC AAT TAT GGA TAT CAT AAT CCA CAA AAT CCA AAA
 Gly Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala Gln Asn Ala Lys
 1375 1380 1385 1390

 TTA GTT GGC GTA AAT ATA ACT GCA CAA TTA GAT TTT AAT GGT TTA TGG
 Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn Gly Leu Trp
 1395 1400 1405

FIG.4P.

AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT AAC CAA GTA
 Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr Asn Gln Val
 1410 1415 1420

AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTA GCC TCC GTA AGC AGT
 Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser Val Ser Ser
 1425 1430 1435

TAT TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC ATT GGT TTA GGC
 Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile Gly Leu Gly
 1440 1445 1450

TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG TTT ACT CAA
 Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met Phe Thr Gln
 1455 1460 1465 1470

TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT GCA TTA GGT
 Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg Ala Leu Gly
 1475 1480 1485

AAC AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT CGG GCA TGG
 Asn Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr Arg Ala Trp
 1490 1495 1500

FIG.4Q.

CAT ATC TTA GAT GTA TCG CGT TAT TAC ATG GCG AAT AAA AAT ATT ATG
His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys Asn Ile Met
1505 1510 1515

CTT CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CGC TAT GTT ACT TGG
Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr Val Thr Trp
1520 1525 1530

GAA GCG GTG CGT CAA ACA GCA CAA GGT GCG GTC AAT CAA CAT CAA AAT
Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln His Gln Asn
1535 1540 1545 1550

GTT GGT AGC TAT ACT CGC TAC GCA GCA TCA GGA AAC TAT ACC TTA
Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn Tyr Thr Leu
1555 1560 1565

ACA TTA GAA ATG AAA TTC TAAATTAAAA TGGGCCAGAT GGACTAGATA
Thr Leu Glu Met Lys Phe
1570

TGCTATATCT ATACCTTACT GCGGCACTT TTTCIGTCT ATAACTGCT TAAGTAAAA

ACCAAACTTG GATTTTTTAC AAGATCTTTT CACACATTTA TTG

FIG. 5A.

ATTGTTTGA CGCATTTT CATATTTAT CCATGAACCTT AAAAAACCTT AACTTGACAT⁻³⁵

TATTACAAA AAAGATCAAT⁻¹⁰ AATCGAATT ATTATCAATT TTGTAAGCT ATATAATTCT²⁰⁵

ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser
1 5 10 15

GCT TGT AGC GGA GGG GGT TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC
Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr
20 25 30

CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA AAA
Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys
35 40 45

AAA TCT AAT TTG AAA AAG TTG TTC ATT CCT TCT TTA GGA GGA GGT ATG
Lys Ser Asn Leu Lys Lys Leu Phe Ile Pro Ser Leu Gly Gly Met
50 55 60

AAA TTG GTG GCT CAG AAT CTT CGT GGT AAT AAA GAA CCT AGT TTC TTA
Lys Leu Val Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu
65 70 75 80

FIG. 5B.

AAT GAA GAT GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ACG ATT GAA
 Asn Glu Asp Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu
 85 90 95

AAG GAT GTT AAA GAT AAC AAT AAA AAC GCG GCG GAC CTT ATT GCG TCA
 Lys Asp Val Lys Asp Asn Asn Lys Asn Gly Ala Asp Leu Ile Gly Ser
 100 105 110

ATA GAC GAG CCT AGT ACA ACA AAT CCA CCC GAA AAG CAT CAT GGA CAA
 Ile Asp Glu Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln
 115 120 125

AAA TAT GTA TAT TCA GCG CTT TAT TAT ACT CCA TCG TCG AGT TTA AAC
 Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Thr Pro Ser Trp Ser Leu Asn
 130 135 140

GAT TCT AAA AAC AAG TTT TAT TTA GGT TAC TAT GGA TAT GCG TTT TAT
 Asp Ser Lys Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr
 145 150 155 160

TAT GGT AAT AAA ACT GCA ACA AAC TTG CCA GTA AAC GGT GTA GCT AAA
 Tyr Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys
 165 170 175

FIG.5C.

TAC AAA GGA ACT TGG GAT TTC ATC ACT GCA ACT AAA AAT GGC AAA CGT
Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg
180 185 190

TAT CCT TTG TTA AGT AAT GGC AGT CAC GCT TAT TAT CGA CGT AGT GCA
Tyr Pro Leu Leu Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala
195 200 205

ATT CCA GAA GAT ATT GAT TTA GAA AAT GAT TCA AAG AAT GGT GAT ATA
Ile Pro Glu Asp Ile Asp Leu Glu Asn Asp Ser Lys Asn Gly Asp Ile
210 215 220

GGC TTA ATA AGT GAA TTT AGT GCA GAT TTT GGG ACT AAA AAA CTG ACA
Gly Leu Ile Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr
225 230 235 240

CGA CAA CTG TCT TAC ACC AAA AGA AAA ACT AAT AAT CAA CCA TAT GAA
Gly Gln Leu Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu
245 250 255

AAG AAA AAA CTC TAT GAT ATA GAT GCC GAT ATT TAT AGT AAT AGA TTC
Lys Lys Lys Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe
260 265 270

FIG. 5D.

AGG GGT ACA GTA AAG CCA ACC GAA AAA GAT TCT GAA GAA CAT CCC TTT
 Arg Gly Thr Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe
 275 280 285

ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA
 Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu
 290 295 300

GAA CTA GGG GGG AAA TTT TTA GCT ACG GAT AAC CGA GTT TTT GGG GTA
 Glu Leu Gly Gly Lys Phe Leu Ala Thr Asp Asn Arg Val Phe Gly Val
 305 310 315 320

TTT AGT GCC AAA GAA ACG GAA GAA ACA AAA AAG GAA GCG TTA TCC AAG
 Phe Ser Ala Lys Glu Thr Glu Glu Thr Lys Lys Glu Ala Leu Ser Lys
 325 330 335

GAA ACC TTA ATT GAT GGC AAG CTA ATT ACT TTC TCT ACT AAA AAA ACC
 Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr
 340 345 350

GAT GCA AAA ACC AAT GCA ACA ACC AGT ACC GCA GCT AAT ACA ACA ACC
 Asp Ala Lys Thr Asn Ala Thr Thr Ser Thr Ala Ala Asn Thr Thr Thr
 355 360 365

FIG. 5E.

GAT ACA ACC GCC AAT ACA ATA ACC GAT GAA AAA AAC TTT AAG ACG GAA
 Asp Thr Thr Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu
 370 375 380

GAT ATA TCA AGT TTT GGT GAA GCT GAT TAT CTG TTA ATT GAC AAA TAT
 Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Ile Asp Lys Tyr
 385 390 395 400

CCT ATT CCA CTT TTA CCT GAT AAA AAT ACT AAT GAT TTC ATA AGT AGT
 Pro Ile Pro Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser
 405 410 415

AAG CAT CAT ACT GTA GGA AAT AAA CGC TAT AAA GTG GAA GCA TGT TGC
 Lys His His Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Cys
 420 425 430

AGT AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT GAA GAC CCA CTT
 Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu
 435 440 445

AAA GAA AAA GAA ACA GAA ACA GAA ACA GAA ACA GAA AAA GAC AAA GAA
 Lys Glu Lys Glu Thr Glu Thr Glu Thr Glu Thr Glu Lys Asp Lys Glu
 450 455 460

FIG.5F.

AAA GAA AAA GAA AAA GAC AAA GAC AAA GAA AAA CAA ACG GCG GCA ACG
Lys Glu Lys Lys Glu Lys Asp Lys Asp Lys Glu Lys Gln Thr Ala Ala Thr
465 470 475 480

ACC AAC ACT TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT CCC AAG GAC
Thr Asn Thr Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Lys Asp
485 490 495

GAC ATA CCT AAA ACA GGA AGT GCA AAA TAT CAT GGT AGT TGG TTT GGT
Asp Ile Pro Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Trp Phe Gly
500 505 510

TAT ATT ACT GAC GGT AAG ACA TCT TAC TCC CCC AGT GGT GAT AAG AAA
Tyr Ile Thr Asp Gly Lys Thr Ser Tyr Ser Pro Ser Gly Asp Lys Lys
515 520 525

CGC GAT AAA AAT GCT GTC GCC GAG TTT AAT GTT GAT TTT GCC GAG AAA
Arg Asp Lys Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys
530 535 540

AAG CTA ACA GGC GAA TTA AAA CGA CAC GAT ACT GGA AAT CCC GTA TTT
Lys Leu Thr Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe
545 550 555 560

FIG. 5G.

AGT ATT GAG GCA AAC TTT AAT AAT AGT AGT AAT GCC TTC ACT GGT ACA	
Ser Ile Glu Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr	575
	565
GCA ACC GCA ACA AAT TTT GTA ATA GAT GGT AAA AAT AGT CAA AAT AAA	
Ala Thr Ala Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys	590
	580
AAT ACC CCA ATT AAT AAT ACA ACT AAA GTA AAC GCG GCA TTT TAT GGA	
Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly	605
	595
CCT AAG GCT TCT GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAT TCT	
Pro Lys Ala Ser Glu Leu Gly Tyr Phe Thr Tyr Asn Gly Asn Ser	620
	610
ACA GCT ACA AAT TCT GAA AGT TCC TCA ACC GTA TCT TCA TCA TCC AAT	
Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr Val Ser Ser Ser Asn	640
	625
TCA AAA AAT GCA AGA GCT GCA GTT GTC TTT GGT GCG AGA CAA CAA GTA	
Ser Lys Asn Ala Arg Ala Ala Val Val Phe Gly Ala Arg Gln Gln Val	655
	645

FIG. 5H.

GAA ACA ACC AAA TAATGAATA CTAATA ATG ACT AAA AAA CCC TAT TTT	
Glu Thr Lys	Met Thr Lys Lys Pro Tyr Phe
660	665
CGC CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT GTA AAA GCA	
Arg Leu Ser Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr Val Lys Ala	
670	675 680
GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG	
Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser Glu Val	
685	690 695
GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT	
Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser Val Thr	
700	705 710 715
GCA GAA AAA ATA AGA GAT CGT AAA GAT AAT GAA GTA ACT GGA CTT GGC	
Ala Glu Lys Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly Leu Gly	
720	725 730
AAA ATT ATC AAA ACT AGT GAA AGT ATC AGC CGA GAA CAA GTA TTA AAT	
Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val Leu Asn	
735	740 745

FIG. 51.

ATT CGT GAT CTA ACA CGC TAT GAT CCA GGG ATT TCA GTT GTA GAA CAA
 Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu Gln
 750 755 760

GGT CGC GGT GCA AGT TCT GGA TAT TCT ATT CGT GGT ATG GAC AGA AAT
 Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn
 765 770 775

AGA GTT GCT TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA TCT TAT GTA
 Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val
 780 785 790 795

GTG CAA AGC CCT TTA GTT GCT CGT TCA GGA TAT TCT GGC ACT GGT GCA
 Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala
 800 805 810

ATT AAT GAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA AGC AAG
 Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys
 815 820 825

GGG GGG AGT TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT GGT TCT GTA
 Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val
 830 835 840

FIG. 5J.

ACA TTT CAA AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA
Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser
845 850

TGG GGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT
Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe
860 865 870 875

ACC CAT TCT TTA GCT GTA GCA GGA AAA CAA GGT GGA TTT GAA GGG CTA
Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Phe Glu Gly Leu
880 885 890

GCC ATT TAC ACT CAA CGA AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT
Ala Ile Tyr Thr Gln Arg Asn Ser Ile Glu Thr Gln Val His Lys Asp
895 900 905

GCA TTA AAA GGC GTA CAA AGT TAT GAT CGA TTA ATC GCC ACA ACA GAT
Ala Leu Lys Gly Val Gln Ser Tyr Asp Arg Leu Ile Ala Thr Thr Asp
910 915 920

AAA TCT TCA GGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT GGT GAT
Lys Ser Ser Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn Gly Asp
925 930 935

FIG.5K.

GAC AAG TGT GCA GCC AAG CCA CCT GCG ACT TTA TCC ACC CAA AGC GAA
 Asp Lys Cys Ala Ala Lys Pro Pro Ala Thr Leu Ser Thr Gln Ser Glu
 940 945 950 955

ACC GTA AGC GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA CCT AAT
 Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn
 960 965 970

CCA ATG AAA TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GGG TAT CAT
 Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Gly Tyr His
 975 980 985

TTT TCT GAA CAA CAT TAT ATT GGT GGT ATT TTT GAA TTC ACA CAA CAA
 Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln
 990 995 1000

AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGC CCA ACA
 Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Ser Pro Thr
 1005 1010 1015

GAA AGA CCG GAT GAT AGT AGT CGT TCT TTT TAT CCA ATG CAA GAT CAT
 Glu Arg Arg Asp Asp Ser Ser Arg Ser Phe Tyr Pro Met Gln Asp His
 1020 1025 1030 1035

FIG.5L.

GGT GCA TAT CAA CAT ATT GAG GAT GGC AGA GGC GTT AAA TAT CCA AGT
Gly Ala Tyr Gln His Ile Glu Asp Gly Arg Gly Val Lys Tyr Ala Ser
1040 1045 1050

GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT ATT GAA
Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu
1055 1060 1065

TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA GCA GTG
Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val
1070 1075 1080

TTA AGT GCT AAT CAA CAA AAC AAC ATC ATA CTT GAC AGT TAT ATG CCA CAT
Leu Ser Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Arg His
1085 1090 1095

ACG CAT TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CCG CCA ACA
Thr His Cys Ser Leu Tyr Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr
1100 1105 1110 1115

CTT GAT AAA CCT TAT TCA TAC TAT CGT TCT GAT AGA AAT GTT TAT AAA
Leu Asp Lys Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val Tyr Lys
1120 1125 1130

FIG. 5M.

GAA AAA CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT CAA CAA
 Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln
 1135 1140 1145

AAT TCG CTT ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT GAC TTT
 Asn Trp Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe
 1150 1155 1160

ACT TCA GCG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ATC GCT
 Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Ile Ala
 1165 1170 1175

ACG GCA GAT AGT ATT CCA AGG AAA CCT GGT GAA ACT GGT AAA CCA AGA
 Thr Ala Asp Ser Ile Pro Arg Lys Pro Gly Glu Thr Gly Lys Pro Arg
 1180 1185 1190 1195

AAT GGT TTG CAA TCA CAA CCT TAC TTA TAC CCA AAA CCA GAG CCA TAT
 Asn Gly Leu Gln Ser Gln Pro Tyr Leu Tyr Pro Lys Pro Glu Pro Tyr
 1200 1205 1210

TTT GCA GGA CAA GAT CAT TGT AAT TAT CAA GGT AGC TCC TCT AAT TAC
 Phe Ala Gly Gln Asp His Cys Asn Tyr Gln Gly Ser Ser Asn Tyr
 1215 1220 1225

FIG.5N.

AGA GAC TGT AAA GIG CCG TTA ATT AAA GCG AAA AAT TAT TAT TTC GCA
Arg Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala
1230 1235 1240

GCA CCG AAT AAT ATG GCA TTA GCG AAA TAC GTT GAT TTA GGT TTA GGT
Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly
1245 1250 1255

ATT CCG TAT GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT
Ile Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser
1260 1265 1270 1275

GTT GGT AAA TTT AAA AAT TTC TCT TGG AAT ACT GGT ATT GTC ATA AAA
Val Gly Lys Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys
1280 1285 1290

CCA ACG GAA TGG CTT GAT CTT TCT TAT CCG CTT TCT ACT GGA TTT AGA
Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg
1295 1300 1305

AAT CCT AGT TTT TCT GAA ATG TAT GGT TGG CCG TAT GGT GCG AAG AAT
Asn Pro Ser Phe Ser Glu Met Tyr Gly Trp Arg Tyr Gly Gly Lys Asn
1310 1315 1320

FIG.50.

GAC GAG GGT TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA	
Asp Glu Val Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln	
1325	1330 1335
GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT	
Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser	
1340	1345 1350 1355
CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT	
His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu	
	1360 1365 1370
AGT AAA AAT GGA ACT GGA AAG GGC AAT TAT GGA TAT CAT AAT GCA CAA	
Ser Lys Asn Gly Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala Gln	
1375	1380 1385
AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCA CAA TTA GAT TTT AAT	
Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn	
1390	1395 1400
GGT TTA TGG AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT	
Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr	
	1405 1410 1415

FIG.5P.

AAC CAA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTA GCC TCC
Asn Gln Val Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser
1420 1425 1430 1435

GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC GGT TAT ATC ATT
Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile
1440 1445 1450

GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG
Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met
1455 1460 1465

TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT
Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg
1470 1475 1480

GCA TTA GGT AAC AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT
Ala Leu Gly Asn Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr
1485 1490 1495

CGG GCA TGG CAT ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT AAA
Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys
1500 1505 1510 1515

FIG. 5Q.

AAT ATT ATG CTT CGA TTA GCG ATA TAT AAT TTA TTC AAC TAT CGC TAT
 Asn Ile Met Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr
 1520 1525 1530

GTT ACT TGG GAA GCG GTG CGT CAA ACA GCA CAA GGT GCG GTC AAT CAA
 Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln
 1535 1540 1545

CAT CAA AAT GTT GGT AGC TAT ACT CGC TAC GCA GCA TCA GGA CGA AAC
 His Gln Asn Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn
 1550 1555 1560

TAT ACC TTA ACA TTA GAA ATG AAA TTC TAAATTAAAA TCGGCCAGAT
 Tyr Thr Leu Thr Leu Glu Met Lys Phe
 1565 1570

GGACTAGATA TGCTATATCT ATACCTTACT GCGGCACTTT TTTCIGTCT ATAACTGCT

TAAGTGA AAA ACCAAACTTG GATTTTTTAC AAGATCTTTT CACACATTTA TGTAAAATC

TCCGACAAAT TTGACCG

FIG. 6A.

AAAATTCGGT AATGATAACC CTATAAATGA TAAGAGAGAA AGTGTGTTTGA CGCCATTTTT

CATATTTTAT CCATGAACIT ⁻³⁵ AAAAAATICT AAGTTGACAT ⁻¹⁰ TATTACAAA AAAGAACAAT

AATGCCAATT ATTATCAATT ^{RBS} TTGTATAAGT ATTAATICT ATG AAA TCT GTA CCT

Met Lys Ser Val Pro
1 5

CIT ATC ACT GGT GGA CIT TCC TTT TTA CTA AGC GCT TGT AGC GGG GGA
Leu Ile Thr Gly Gly Leu Ser Phe Leu Leu Ser Ala Cys Ser Gly Gly
10 15 20

GGT GGT TCT TTT GAT GTA GAT GAC GTC TCT AAT CCC TCC TCT TCT AAA
Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro Ser Ser Ser Lys
25 30 35

CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA ACA AAA TCT GAT TTG
Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Thr Lys Ser Asp Leu
40 45 50

GAA AAG TIG TIC ATT CCT TCT TTA GGG GGA GGG ATG AAG TTA GTG CCT
Glu Lys Leu Phe Ile Pro Ser Leu Gly Gly Gly Met Lys Leu Val Ala
55 60 65

FIG.6B.

CAA AAT TTT ATT GGT GCT AGA GAA CCT AGT TTC TTA AAT GAA GAT GGC
Gln Asn Phe Ile Gly Ala Arg Glu Pro Ser Phe Leu Asn Glu Asp Gly
70 75 80 85

TAT ATG ATA TTT TCC TCA CTT TCT ACG ATT GAA GAG GAT GTT GAA AAA
Tyr Met Ile Phe Ser Ser Leu Ser Thr Ile Glu Glu Asp Val Glu Lys
90 95 100

GTT AAA AAT AAC AAT AAA AAC GCG GCG AGG CTT ATT GGC TCA ATT GAG
Val Lys Asn Asn Asn Lys Lys Asn Gly Gly Arg Leu Ile Gly Ser Ile Glu
105 110 115

GAA CCT AAT GGA ACA TCA CAA AAT TCT AAT TCA CAA GAA TAC GTT TAT
Glu Pro Asn Gly Thr Ser Gln Asn Ser Asn Ser Gln Glu Tyr Val Tyr
120 125 130

TCT GGT TTG TAT TAT ATC GAT AGT TGG CGT GAT TAT AAG AAG GAA GAG
Ser Gly Leu Tyr Tyr Ile Asp Ser Trp Arg Asp Tyr Lys Lys Glu Glu
135 140 145

CAA AAA GCT TAT ACT GGC TAT TAT GGT TAT GCA TTT TAT TAT GGT AAT
Gln Lys Ala Tyr Thr Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr Gly Asn
150 155 160 165

FIG. 6C.

GAA ACT GCA AAA AAC TTG CCA GTA AAA GGT GTA GCT AAA TAC AAA GGA
 Glu Thr Ala Lys Asn Leu Pro Val Lys Gly Val Ala Lys Tyr Lys Gly
 170 175 180

ACG TGG AAC TTC ATC ACT GCA ACT GAA AAT GGC AAA CGT TAT TCT TTG
 Thr Trp Asn Phe Ile Thr Ala Thr Glu Asn Gly Lys Arg Tyr Ser Leu
 185 190 195

TTC AGT AAT TCT ATC GGT CAA GCT TAT TCC AGA CGC AGC GCT ATT TCA
 Phe Ser Asn Ser Ile Gly Gln Ala Tyr Ser Arg Arg Ser Ala Ile Ser
 200 205 210

GAA GAT ATC TAT AAT TTA GAA AAC GGT GAC GCG GGC TTA ATA AGT GAA
 Glu Asp Ile Tyr Asn Leu Glu Asn Gly Asp Ala Gly Leu Ile Ser Glu
 215 220 225

TTT AGT GTA GAT TTT GGT AAG AAA GAG CTC ACT GGA GAA CTT TAT TAT
 Phe Ser Val Asp Phe Gly Lys Lys Glu Leu Thr Gly Glu Leu Tyr Tyr
 230 235 240 245

AAT GAA AGG AAA ACA AGT GTT AAT GAA TCA CAA AAT ACA ACA CAT AAA
 Asn Glu Arg Lys Thr Ser Val Asn Glu Ser Gln Asn Thr Thr His Lys
 250 255 260

FIG. 6D.

CTC TAC ACT CTA GAA GCT AAA GTG TAT AGC AAC CGA TTC AGA GGT AAA
 Leu Tyr Thr Leu Glu Ala Lys Val Tyr Ser Asn Arg Phe Arg Gly Lys
 265 270 275

GTA AAG CCA ACC AAA ACA AAG TCT GAA GAT CAT CCC TTT ACC AGC GAG
 Val Lys Pro Thr Lys Thr Lys Ser Glu Asp His Pro Phe Thr Ser Glu
 280 285 290

CGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA GAA CTA GGG
 Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly
 295 300 305

CGA AAG TTT TTA GCT AAC GAC GAA AAA GTT TTT GGG GTA TTT AGT GCC
 Gly Lys Phe Leu Ala Asn Asp Glu Lys Val Phe Gly Val Phe Ser Ala
 310 315 320 325

AAA GAA GAC CCA CAA AAC CCA GAA AAC CAA AAA TTA TCC ACA GAA ACC
 Lys Glu Asp Pro Gln Asn Pro Glu Asn Gln Lys Leu Ser Thr Glu Thr
 330 335 340

TTA ATT GAT GGC AAG CTA ATT ACT TTT AAA AGA ACT GAT GCA ACA ACC
 Leu Ile Asp Gly Lys Leu Ile Thr Phe Lys Arg Thr Asp Ala Thr Thr
 345 350 355

FIG. 6E.

AAT GCA ACA ACC GAT GCA AAA ACC AGT GCA ACA ACC GAT GCA ACC AGT
Asn Ala Thr Thr Asp Ala Lys Thr Ser Ala Thr Thr Asp Ala Thr Ser
360 365 370

ACA ACA GCC AAT AAA AAA ACC GAT GCA GAA AAC TTT AAG ACG GAA GAT
Thr Thr Ala Asn Lys Lys Thr Asp Ala Glu Asn Phe Lys Thr Glu Asp
375 380 385

ATA CCA AGT TTT GGT GAA GCT GAT TAC CTT TTA ATT GGC AAT CAG CCT
Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Gly Asn Gln Pro
390 395 400 405

ATT OCT CTT TTA CCT GAA AAA AAT ACT GAT GAT TTC ATA AGT AGT AAG
Ile Pro Leu Leu Pro Glu Lys Asn Thr Asp Asp Phe Ile Ser Ser Lys
410 415 420

CAC CAT ACG GTA GGA GGT AAA ACC TAT AAA GTA GAA GCA TGT TGC AAG
His His Thr Val Gly Gly Lys Thr Tyr Lys Val Glu Ala Cys Cys Lys
425 430 435

AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT GAG GAT AAA GAT AAG
Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys Asp Lys
440 445 450

FIG. 6F.

GAC AAC AAA AAT GAA ACA GAC AAA GAA AAA GGC AAA GAA AAA CCA ACG
 Asp Asn Lys Lys Asn Glu Thr Asp Lys Glu Lys Gly Lys Glu Lys Pro Thr
 455 460 465

ACG ACA ACA TCT ATC AAC ACT TAT TAT CAA TTC TTA TTA GGT CTC CGT
 Thr Thr Thr Ser Ile Asn Thr Tyr Tyr Gln Phe Leu Leu Gly Leu Arg
 470 475 480 485

ACT CCC AAG GAC GAA ATA CCT AAA GAA GGA AGT CCA AAA TAT CAT GGT
 Thr Pro Lys Asp Glu Ile Pro Lys Glu Gly Ser Ala Lys Tyr His Gly
 490 495 500

AAT TGG TTT GGT TAT ATT AGT GAT GGC GAG ACA TCT TAC TCC GCC AGT
 Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu Thr Ser Tyr Ser Ala Ser
 505 510 515

GGT GAT AAG GAA CCG AGT AAA AAT GCT GTC GCC GAG TTT GAT GTA AGT
 Gly Asp Lys Glu Arg Ser Lys Asn Ala Val Ala Glu Phe Asp Val Ser
 520 525 530

TTT GCC AAT AAA ACA TTA ACA GGC GAA TTA AAA CGA CAC GAT AAT GGA
 Phe Ala Asn Lys Thr Leu Thr Gly Glu Leu Lys Arg His Asp Asn Gly
 535 540 545

FIG. 6G.

AAT ACC GTA TTT AAA ATT AAT GCA GAA TTA AAT GGT AGT AAT GAC TTC	
Asn Thr Val Phe Lys Ile Asn Ala Glu Leu Asn Gly Ser Asn Asp Phe	565
550	560
ACT GGT ACA GCA ACC GCA ACA AAT TTT GTA ATA GAT GGT AAC AAT AGT	
Thr Gly Thr Ala Thr Ala Thr Asn Phe Val Ile Asp Gly Asn Asn Ser	580
570	575
CAA ACT TCA AAT GCC AAA ATT AAT ATT ACA ACT AAA GTA AAT GGG GCA	
Gln Thr Ser Asn Ala Lys Ile Asn Ile Thr Thr Lys Val Asn Gly Ala	595
585	590
TTT TAT GGA CCT AAG GCT TCT GAA TTA GGA GGG TAT TTC ACC TAT AAC	
Phe Tyr Gly Pro Lys Ala Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn	610
600	605
GGA AAA AAT CCT ACA GCT ACA AAT TCT GAA AGT TCC TCA ACC GTA CCT	
Gly Lys Asn Pro Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr Val Pro	625
615	620
TCA CCA CCC AAT TCA CCA AAT GCA AGC GCT GCA GTT GTC TTT GGT GCT	
Ser Pro Pro Asn Ser Pro Asn Ala Ser Ala Ala Val Val Phe Gly Ala	645
630	635

FIG.6H.

AAA AAA CAA GTA GAA ACA ACC AAC AAG TAAAAACAAC CAAGTAATGG

Lys Lys Gln Val Glu Thr Thr Asn Lys

650

AATACTAAAA ATG ACT AAA AAA CCC TAT TTT CGC CTA AGT ATT ATT TCT

Met Thr Lys Lys Pro Tyr Phe Arg Leu Ser Ile Ile Ser

655

660

665

TGT CTT TTA ATT TCA TGC TAT GTA AAA GCA GAA ACT CAA AGT ATA AAA

Cys Leu Leu Ile Ser Cys Tyr Val Lys Ala Glu Thr Gln Ser Ile Lys

670

675

680

GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG GAC ACT CAA AGT ACA GAA

Asp Thr Lys Glu Ala Ile Ser Ser Glu Val Asp Thr Gln Ser Thr Glu

685

690

695

GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT GCA GAA AAA ATA AGA GAT

Asp Ser Glu Leu Glu Thr Thr Ile Ser Val Thr Ala Glu Lys Ile Arg Asp

700

705

710

715

CGT AAA GAT AAT GAA GTA ACT GGA CTT GGC AAA ATT ATC AAA ACT AGT

Arg Lys Asp Asn Glu Val Thr Gly Leu Gly Lys Ile Ile Lys Thr Ser

720

725

730

FIG. 61.

GAA AGT ATC AGC CGA GAA CAA GTA TTA AAT ATT CGT GAT CTA ACA CGC
 Glu Ser Ile Ser Arg Glu Gln Val Leu Asn Ile Arg Asp Leu Thr Arg
 735 740 745

TAT GAT CCA GGC ATT TCA GTT GTA GAA CAA GGC CGT GGT GCA AGT TCT
 Tyr Asp Pro Gly Ile Ser Val Val Glu Gln Gly Arg Gly Ala Ser Ser
 750 755 760

GGA TAT TCT ATT CGT GGT ATG GAC AGA AAT AGA GTT GCT TTA TTA GTA
 Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn Arg Val Ala Leu Leu Val
 765 770 775

GAT GGT TTA CCT CAA ACG CAA TCT TAT GTA GTG CAA AGC CCT TTA GTT
 Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val Val Gln Ser Pro Leu Val
 780 785 790 795

GCT CGT TCA GGA TAT TCT GGC ACT GGT GCA ATT AAT GAA ATT GAA TAT
 Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala Ile Asn Glu Ile Glu Tyr
 800 805 810

GAA AAT GTA AAG GCC GTC GAA ATA ACG AAG GCG GCG AGT TCT TCT GAG
 Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Gly Ser Ser Ser Glu
 815 820 825

FIG. 6J.

TAT GGT AAT GGA GCA CTA GCT GGT TCT GTA ACA TTT CAA AGC AAA TCA
Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Thr Phe Gln Ser Lys Ser
830 835

GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA TGG GGA ATT CAA ACT AAA
Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser Trp Gly Ile Gln Thr Lys
845 850

AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT ACC CAT TCT TTA GCT GTA
Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe Thr His Ser Leu Ala Val
860 865 870 875

GCT CGA AAA CAA GGG GGA TTT GAC GGG GTC GCC ATT TAT ACT CAA CGA
Ala Gly Lys Gln Gly Gly Phe Asp Gly Val Ala Ile Tyr Thr Gln Arg
880 885 890

AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT GCA TTA AAA GGC GTA CAA
Asn Ser Ile Glu Thr Gln Val His Lys Asp Ala Leu Lys Gly Val Gln
895 900 905

AGT TAT CAT CGA TTA ATC GCC AAA CCA GAG GAT CAA TCT GCA TAC TTT
Ser Tyr His Arg Leu Ile Ala Lys Pro Glu Asp Gln Ser Ala Tyr Phe
910 915 920

FIG. 6K:

GTG ATG CAA GAT GAG TGT CCA AAG CCA GAT GAT TAT AAC AGT TGT TTA
Val Met Gln Asp Glu Cys Pro Lys Pro Asp Asp Tyr Asn Ser Cys Leu
925 . 930 935

CCT TTC GCC AAA CGA CCT GCG ATT TTA TCC TCC CAA AGA GAA ACC GTA
Pro Phe Ala Lys Arg Pro Ala Ile Leu Ser Ser Gln Arg Glu Thr Val
940 945 950 955

AGC GTT TCA GAT TAT ACG GGT AAC CGT ATC AAA CCT AAT CCA ATG
Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn Pro Met

AAA TAT GAA AGC CAG TCT TCG TTT TTA AGA GGA GGG TAT CAT TTT TCT
Lys Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Tyr His Phe Ser

GAA CAA CAT TAT ATT GGT GGT TTT GAA TTC ACA CAA AAA TTT
Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln Lys Phe

990 995 1000

GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGA TCA ACA GAA AAA
Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Arg Ser Thr Glu Lys

TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA CGT GAT
Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr Arg Asp
1100 1105 1110 1115

AAA CCT TAT TCA TAC TAT CAT TCT GAT AGA AAT GTT TAT AAA GAA AAA
Lys Pro Tyr Ser Tyr Tyr His Ser Asp Arg Asn Val Tyr Lys Glu Lys

CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT CAA CAA AAT TGG
His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Asn Trp

1135 1140 1145

CTT ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT GAC TTT ACT TCA
Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe Thr Ser

CGC CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ACC GCT ACG GCA
Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Thr Ala Thr Ala
1165 1170 1175

AAAG AGT ATT TCA GAG AAA GCT AAT GAA ACA AGA AAT GGT TAC AAA
Lys Ser Ile Ser Glu Lys Ala Asn Glu Thr Arg Arg Asn Gly Tyr Lys
1180 1185 1190 1195

AAA CAA CCT TAC TTA TAC CCA AAA CCA ACA GTA GGT TTT GTA GTA CAA
Lys Gln Pro Tyr Leu Tyr Pro Lys Pro Thr Val Gly Phe Val Val Gln

FIG. 6N.

GAT CAT TGT GAT TAT AAA GGT AAC TCC TCT AAT TAC AGA GAC TGT AAA	
Asp His Cys Asp Tyr Lys Gly Asn Ser Ser Asn Tyr Arg Asp Cys Lys	1215 1220 1225
GTG CCG TTA ATT AAA GCG AAA AAT TAT TAT TIC GCA GCA CCG AAT AAT	
Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala Ala Arg Asn Asn	1230 1235 1240
ATG GCA TTA GCG AAA TAC GTT GAT TTA GGT TTA GGT ATT CCG TAT GAC	
Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly Ile Arg Tyr Asp	1245 1250 1255
GTA TCT CCG ACA AAA GCT AAT GAA TCA ACT ATT AGT GTT GGT AAA TTT	
Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser Val Gly Lys Phe	1260 1265 1270 1275
AAA AAT TTC TCT TCG AAT ACT GGT ATT GTC ATA AAA CCA ACG GAA TGG	
Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys Pro Thr Glu Trp	1280 1285 1290
CTT GAT CTT TCT TAT CCG CTT TCT ACT GGA TTT AGA AAT CCT AGT TTT	
Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg Asn Pro Ser Phe	1295 1300 1305

FIG. 60.

GCT GAA ATG TAT GGT TGG CCG TAT GGT GGC AAT AAT AGC GAG GTT TAT
Ala Glu Met Tyr Gly Trp Arg Tyr Gly Gly Asn Asn Ser Glu Val Tyr
1310 1315 1320

GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA GAG TTT GGT CTC
Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln Glu Phe Gly Leu
1325 1330 1335

GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT CAT TTT AGT AAT
Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser His Phe Ser Asn
1340 1345 1350 1355

GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT AAT AAA AAT GGA
Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu Asn Lys Asn Gly
1360 1365 1370

ACT GGA AAG GCC AAT TAT GGA TAT CAT AAT GCA CAA AAT GCA AAA TTA
Thr Gly Lys Ala Asn Tyr Gly Tyr His Asn Ala Gln Asn Ala Lys Leu
1375 1380 1385

GTT GGC GTA AAT ATA ACT GCG CAA TTA GAT TTT AAT GGT TTA TGG AAA
Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn Gly Leu Trp Lys
1390 1395 1400

FIG. 6P.

CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT AAC CGA GTA AAA
 Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr Asn Arg Val Lys
 1405 1410 1415

GTT AAA GAT CAA AAA ATC AAT GCT GGT TTG GCC TCC GTA AGC AGT TAT
 Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser Val Ser Ser Tyr
 1420 1425 1430 1435

TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC ATT GGT TTA GGC TAT
 Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile Gly Leu Gly Tyr
 1440 1445 1450

GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG TTT ACT CAA TCA
 Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met Phe Thr Gln Ser
 1455 1460 1465

AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT GCA TTG GGT AAC
 Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg Ala Leu Gly Asn
 1470 1475 1480

AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT CGG GCA TGG CAT
 Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr Arg Ala Trp His
 1485 1490 1495

CACTTTTTC TC TATTACAAA ACAATAAGGA TCCTTTTGIG AATCTCTCA

FIG.7 A.

CAACATCTGC CCAAGCTATA TTGGTTAATG ATAAGCTAT TAAIGATAAG CCTATTATATG

ATAAGAAAGA AATTIGTTTT ACCCATTTT TCATATTTTA TCCAAGAACT TAAAAAATTC

TAAGTIGACA TTATTACAAA AAAAGAACAA TAATGCGAAT TATTATCAAT TTGTATATAAG

AATATAATTC T ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT

Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe

1 5 10

TTA TTA AGT GCT TGT AGC GGA GGA GGG TCT TTT GAT GTA GAT AAC GTC

Leu Leu Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val

15 20 25

TCT AAT CCC TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT

Ser Asn Pro Ser Ser Lys Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn

30 35 40 45

CAA AGA ACA AAA TCT GAT TTG CAA AAG TTG TCC ATT CCT TCT TTA GGG

Gln Arg Thr Lys Ser Asp Leu Leu Lys Leu Ser Ile Pro Ser Leu Gly

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FIG. 7C.

ACT TTG GCA AGC AAA CAG CCA CTA CAT TAC CTG TAGATGGCGA AGCAACGTAT
 Thr Leu Ala Ser Lys Gln Pro Leu His Tyr Leu

160 165

AAAGGAACIT GGCACITTCAT CACCGCAACT GAAATGGCA AAAAGTATTC TTGTTTCAGT
 AATGATAGCG GTCAAGCTTA TCGCAGACGT AGTCCAATTC CAGAAGATAT TGATTTAGAA
 AAAAATGATT CAACTAATGG TGACAAGGCG TTAATAAGTG AATTTAGTGT CAATTITGGT
 ACAAAAAAGC TCACIGGAAA ACTTTATTAT AATCAAAAGAG AAACAGAACT TAATAAATCA
 AAAGATAGAA AACATACACT CTACAACTTA GAAGCTGAAG TGTATAGTAA CCGATTTCAGG
 GGTACAGTAA AGCCAACCGA AAAAGATTCT ACAGATCATC CCTTTACCAG CGAGGGAACA
 TTAGAAGGIG GTTTTTATGG GCCTAAAGGT GAAGAACTAG GAGGAAAGTT TTTAGCTGGC
 GATAAAAAAG TTTTITGGGT ATTTAGTGCC AAAGAAACGG AAGAAACAAA AAAGAAAGCG
 TTATCCAAGG AAACCTTAAT TGATGGCAAG CTAACTACTT TTAAACAAC CAATGCCAACA
 ACCAATGCCA CAGCCAATGC AACAAACCAGT ACAACAGCCA GTACAACAAC CGATGCCAGAA

FIG. 7D.

AACTTTACGA CGAAAGATAT ACCAAGTTTT GGIGAAGCIG ATTACCTTTT AATIGATAAT
 TACCCIGTTC CTCCTTTTACC TGAGAGTGGT GATTTCATAA GTAGTAAGCA CCATACGTGA
 GGAAAGAAA CCTATCAAGT AGAAGCATGT TCCAGTAATC TAAGCTATGT GAAATTIGGT
 ATGTTTTATG AAGACCCACT TAAAGAAGAA AAAGACAAAG AAAAGAAGA AGACAAAGAA
 AAACAAACCG CGCAACGAC CAACACTTAT TATCAATTCT TATTAGGTCT CCGTACTGCC
 AGTTCIGAAA TTCTTAAAT GCGAAACGIG GAATATCGCG GTAAATGGTT TGGTTATATT
 AGTGATGGCA CGACATCTTA CTCCTCCAGT GGIGATAAGG AACCCAATAA AAATGCTCCC
 GCGGATTTTA ATGTTGATTT TGICAATAAA AAGCTAACAG GCACATTAAA ACGACACGAT
 AATGGAAATA CCGTATTTAG TATTGAGGCA AACTTTAACA GTCGGAATGA CTTCACGTGT
 AAAGCAACCG CAAAAGATTT AGTAATAGAT GGTAATAAGTA CACAAGCCAC ATCTAAAGTC
 AATTTCACCG CAACAGTAAA AGGGCCATTT TATGGACCIG ATGCTTCIGA ATTAGGGGGT
 TATTTCACCT ATAACGGAAA AAATCTTACA GCTACAAATT CCCCACCGT ATCTTCACCA

FIG. 7F.

TTA AAT ATT CGT GAT CTA ACA CGC TAT GAT CCA CGC ATT TCA GTT GTA
Leu Asn Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val
255 260 265

GAA CAA GGT CGC GGT GCA AGT TCT CGA TAT TCT ATT CGT GGT ATG GAC
Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp
270 275 280 285

AGA AAT AGA GTT GCT TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA TCT
Arg Asn Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln Ser
290 295 300

TAT GTA GTG CAA AGC CCT TTA GTT GCT CGT TCA GGA TAT TCT GGC ACT
Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr
305 310 315

CGT GCA ATT AAT GAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA
Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile
320 325 330

AGC AAG GGG GGT AGT TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT GGT
Ser Lys Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly
335 340 345

FIG.76.

TCT GTA ACA TTT CAA AGC AAA TCC GCA GCC GAT ATC TTA GAA GGA GAC

Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp
350 355 360 365

AAA TCA TCG CGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA
Lys Ser Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys
370 375 380

GGC TTT ACC CAT TCT TTA GCT GTA GCA GGA AAA CAA GGT GGA TTT GAA
Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu
385 390 395

GGG GTC GCC ATT TAC ACT CAA CGA AAT TCG GAG GAA ACC CAA GTC CAT
Gly Val Ala Ile Tyr Thr Gln Arg Asn Ser Glu Glu Thr Gln Val His
400 405 410

AAA GAT GCA TTA AAA GGC GTA CAA AGT TAT GAG CGA TTC ATC GCC ACA
Lys Asp Ala Leu Lys Gly Val Gln Ser Tyr Glu Arg Phe Ile Ala Thr
415 420 425

ACA GAT AAA TCT TCA GGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT
Thr Asp Lys Ser Ser Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn
430 435 440 445

FIG.7H.

GGT GAT GAC AAG TGT GCA GCC AAA CCA CCT GCA AAG TTA TCC CCC CAA
Gly Asp Lys Cys Ala Ala Lys Pro Pro Ala Lys Leu Ser Pro Gln
450 455 460

AGC GAA ACC GTA AGC GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA
Ser Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys
465 470 475

CCT AAT CCA ATG AAA TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GGG
Pro Asn Pro Met Lys Tyr Glu Ser Glu Ser Trp Phe Leu Arg Gly Gly
480 485 490

TAT CAT TTT TCT GAA CAA CAC TAT ATT GGT GGT ATT TTT GAA TTC ACA
Tyr His Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr
495 500 505

CAA CAA AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGA
Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Arg
510 515 520 525

TCA ACA GAA AAA CGG GAT GAT AGA ACT GGC CCT TTT TAT CCA AAG CAA
Ser Thr Glu Lys Arg Asp Arg Thr Gly Pro Phe Tyr Pro Lys Gln
530 535 540

FIG. 71.

GAT TAT GGT GCA TAT CAA CGT ATT GAG GAT GGC CGA GGC GTT AAC TAT
Asp Tyr Gly Ala Tyr Gln Arg Ile Glu Asp Gly Arg Gly Val Asn Tyr
545 550 555

GCA AGT GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT
Ala Ser Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly
560 565 570

ATT GAA TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA
Ile Glu Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys
575 580 585

GCA GIG TTA AGT GCT AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG
Ala Val Leu Ser Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met
590 595 600 605

CGA CAT ACG CAT TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC
Arg His Thr His Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg
610 615 620

CCG ACA CTT GAT AAA CCT TAT TCA TAC TAT CGT TCT GAT AGA AAT GTT
Pro Thr Leu Asp Lys Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val
625 630 635

FIG. 7J.

TAT AAA GAA AAA CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT
Tyr Lys Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile
640 645 650

CAA CAA AAT TGG CTT ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT
Gln Gln Asn Trp Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp
655 660 665

GAC TTT ACT TCA GCG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GGT
Asp Phe Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val
670 675 680 685

ACC GCT ACG GCA AAT AAT ATT TCA GGG ACA GTT GCT GGT AAA CGA AGA
Thr Ala Thr Ala Asn Ile Ile Ser Gly Thr Val Ala Gly Lys Arg Arg
690 695 700

AAT GGT TAC GAA AAA CAA CCT TAC TTA TAC TCA AAA CCA AAA GTA GAT
Asn Gly Tyr Glu Lys Gln Pro Tyr Leu Tyr Ser Lys Pro Lys Val Asp
705 710 715

TTT GTA CGA CAA GAT CAT TGT AAT TAT AAA GGT AGC TCC TCT AAT TAC
Phe Val Gly Gln Asp His Cys Asn Tyr Lys Gly Ser Ser Ser Asn Tyr
720 725 730

AGC GAC TGT AAA GTG CCG TTA ATT AAA GGG AAA AAT TAT TAT TTC GCA
Ser Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala

GCA CGC AAT AAT ATG GCA TTA GGG AAA TAC ATT GAT TTA GGT TTA GGT
 Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Ile Asp Leu Gly Leu Gly
 750 755 760 765

ATT CGG TAT GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT
Ile Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser
770 775 780

GTT GGT AAA TTT AAA AAT TTC TCT TCG AAT ACT GGT ATT GTC ATA AAA
 Val Gly Lys Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys

CCA ACG GAA TGG CTT GAT CTT TCT TAT TAT CGC CTT TCT ACT GGA TTT AGA
Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg

AAT CCT AGT TTT GCT GAA ATG TAT GGT TGG CCG TAT GGT GGC AAT AAT
Asn Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Tyr Gly Gly Asn Asn

FIG. 7L.

AGC GAT GTT TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA
Ser Asp Val Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln
830 835 840 845

GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT
Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser
850 855 860

CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT
His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu
865 870 875

AGT AAA AAT GGA ACT ACT CGA AAG GGC AAT TAT GGA TAT CAT AAT GCA
Ser Lys Asn Gly Thr Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala
880 885 890

CAA AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCG CAA TTA GAT TTT
Gln Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe
895 900 905

AAT GGT TTA TGG AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT
Asn Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala
910 915 920 925

FIG. 7M.

TAT AAC CGA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTG GCC
Tyr Asn Arg Val Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala
930 935 940

TCC GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC GGT TAT ATC
Ser Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile
945 950 955

ATT GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA
Ile Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr
960 965 970

ATG TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA CAA
Met Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Gln
975 980 985

CGT GCA TTG GGT AAC AAT TCA AGG AAT GTA AAA TCA ACA AGA AAA CTT
Arg Ala Leu Gly Asn Asn Ser Arg Asn Val Lys Ser Thr Arg Lys Leu
990 995 1000 1005

ACT CGG GCA TGG CAT ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT
Thr Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn
1010 1015 1020

FIG. 8A.

AT ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA TTA
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu
1 5 10 15

AGT GCT TGT AGC GGG GGA GGT GGT TCT TTT GAT GTA GAT GAC GTC TCT
Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser
20 25 30

AAT CCC TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT TCA AGT TCA
Asn Pro Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser
35 40 45

AGA ACA AAA TCT AAA TTG GAA AAT TTG TCC ATT CCT TCT TTA GGG GGA
Arg Thr Lys Ser Lys Leu Glu Asn Leu Ser Ile Pro Ser Ser Leu Gly Gly
50 55 60

GGG ATG AAG TTA GTG GCT CAG AAT CTT CGT GAT AGG ACA AAA CCT AGT
Gly Met Lys Leu Val Ala Gln Asn Leu Arg Asp Arg Thr Lys Pro Ser
65 70 75

CTC TTA AAT GAA GAT GAC TAT ATG ATA TTT TCC TCA CTT TCA ACG ATT
Leu Leu Asn Glu Asp Asp Tyr Met Ile Phe Ser Ser Ser Leu Ser Thr Ile
80 85 90 95

AAA GCT GAT GTT GAA AAA GAA AAT AAA CAC TAT ACA AGT CCA GTT GGC
Lys Ala Asp Val Glu Lys Glu Asn Lys His Tyr Thr Ser Pro Val Gly

TCA ATA GAC GAG OCT AGT ACA ACA AAT CCA AAA GAA AAT GAT CAT GGA
Ser Ile Asp Glu Pro Ser Thr Thr Asn Pro Lys Glu Asn Asp His Gly

CAA AGA TAT GTA TAT TCA GGA CTT TAT TAT ATT CCA TCG TCG AAT TTA
Gln Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp Asn Leu
130 135 140

AAC GAT CTT AAA AAT AAC AAG TAT TAT TCT GGT TAC TAT GGA TAT
Asn Asp Leu Lys Asn Asn Lys Tyr Tyr Tyr Ser Gly Tyr Tyr Gly Tyr
145 150 155

GGG TAT TAC TTT GGC AAG CAA ACA GGC ACT ACA TTA CCT GTA AAT GGC
Ala Tyr Tyr Phe Gly Lys Gln Thr Thr Ala Thr Thr Leu Pro Val Asn Gly
160 165 170 175

AAA GTA ACG TAT AAA GGA ACT TGG AGC TTC ACC GCA GCT GAA AAT
Lys Val Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn
180 185 190

FIG. 8C.

GGC AAA AGG TAT OCT TTG TTA AGT AAT GGC AGT CAA GCT TAT TTT CGA
Gly Lys Arg Tyr Pro Leu Ser Asn Gly Ser Gln Ala Tyr Phe Arg
195 200 205

CGT AGT GCA ATT CCA GAA GAT ATT GAT TTA GAA GTT AAA AAT GAT GAG
Arg Ser Ala Ile Pro Glu Asp Ile Asp Leu Glu Val Lys Asn Asp Glu
210 215 220

AAT AGA GAA AAA GGG CTA GTG AGT GAA TTT AGT GCA GAT TTT GGG ACT
Asn Arg Glu Lys Gly Leu Val Ser Glu Phe Ser Ala Asp Phe Gly Thr
225 230 235

AAA AAA CTG ACA GGA GGA CTG TTT TAC ACC AAA AGA CAA ACT CAT ATT
Lys Lys Leu Thr Gly Gly Leu Phe Tyr Thr Lys Arg Gln Thr His Ile
240 245 250 255

CAA AAC CAT GAA AAG AAA AAA CTC TAT GAT ATA GAT GCC CAT ATT TAT
Gln Asn His Glu Lys Lys Lys Leu Tyr Asp Ile Asp Ala His Ile Tyr
260 265 270

AGT AAT AGA TTC AGA GGT AAA GTA AAT AAT CCT ACC CAA AAA GAT TCT AAA
Ser Asn Arg Phe Arg Gly Lys Val Asn Pro Thr Gln Lys Asp Ser Lys
275 280 285

FIG.8D.

GAA CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAC GGG
Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly
290 295 300

CCT GAA GGT CAA GAA TTA GGA GGA AAG TTT TTA GCT GGC GAC AAA AAA
Pro Glu Gly Gln Glu Leu Glu Gly Gly Lys Phe Leu Ala Gly Asp Lys Lys
305 310 315

GTT TTT GGG GTA TTT AGT GCC AAA GGA ACG GAA GAA AAC AAA AAA TTA
Val Phe Gly Val Phe Ser Ala Lys Gly Thr Glu Glu Asn Lys Lys Leu
320 325 330 335

CCC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT ACT AAA
Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr Lys
340 345 350

ACA ACC GAT GCA AAA ACC AAT GCA ACA GCC AAT GCA ACA ACC AGT ACC
Thr Thr Asp Ala Lys Thr Asn Ala Thr Ala Asn Ala Thr Thr Ser Thr
355 360 365

GCA GCC AAT ACA ACA ACC GAT ACA ACA GCC AAT ACA ATA ACC GAT GCA
Ala Ala Asn Thr Thr Thr Asp Thr Thr Ala Asn Thr Ile Thr Asp Ala
370 375 380

FIG.8E.

GAA AAC TTT AAG ACG AAA GAT ATA TCA AGT TTT GGT GAA GCT GAT TAC
 Glu Asn Phe Lys Thr Lys Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr
 385 390 395

CTT TTA ATT GAT AAT TAC CCT GGT CCT CTT TTA CCT GAG AGT GGT GAT
 Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu Ser Gly Asp
 400 405 410 415

TTC ATA AGT AGT AAG CAC CAT ACT GTA GGA AAG AAA ACC TAT CAA GTA
 Phe Ile Ser Ser Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val
 420 425 430

AAA GCA TGT TGC AGT AAT CTA AGC TAT GIG AAA TTT GGT ATG TAT TAT
 Lys Ala Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr
 435 440 445

GAA GTC CCA CCT AAA GAA GAA GAA GAC AAA GAA AAA GAA AAA
 Glu Val Pro Pro Lys Glu Glu Glu Lys Asp Lys Glu Lys Lys Glu Lys
 450 455 460

GAA AAA GAA AAA CAA GCG ACA AAT CTA TCG AAC ACT TAT TAT CAA TTC
 Glu Lys Glu Lys Lys Gln Ala Thr Asn Leu Ser Asn Thr Tyr Tyr Gln Phe
 465 470 475

FIG.8F.

TTA TTA GGT CTC CGT ACT CCC AGT TCT GAA ATT CCT AAA GGA GGA AGT	
Leu Leu Gly Leu Arg Thr Pro Ser Ser Glu Ile Pro Lys Gly Gly Ser	
480	485 490 495
GCA AAA TAT CTC GGT AGT TGG TTT GGT TAT CTG AGC GAT GGT TCA ACA	
Ala Lys Tyr Leu Gly Ser Trp Phe Gly Tyr Leu Ser Asp Gly Ser Thr	
500	505 510
TCT TAC TCC CCC AGT GGT GAT AAG AAA CGC GAG AAC AAT GCT CTC GCC	
Ser Tyr Ser Pro Ser Gly Asp Lys Lys Arg Glu Asn Asn Ala Leu Ala	
515	520 525
GAG TTT AAT GTA AAT TTT GTC GAT AAA ACA TTA AAA GGC CAA TTA ATA	
Glu Phe Asn Val Asn Phe Val Asp Lys Thr Leu Lys Gly Gln Leu Ile	
530	535 540
CGA CAC GAT AAT CAA AAT ACC GTT TTT ACA ATT GAT GCA ACC TTT AAA	
Arg His Asp Asn Asn Gln Asn Thr Val Phe Thr Ile Asp Ala Thr Phe Lys	
545	550 555
GGT GGT AAG AAT AAC TTC ACT GGT ACA GCA ACC GCA AAC AAT GTA GCG	
Gly Gly Lys Asn Asn Phe Thr Gly Thr Ala Thr Ala Asn Asn Val Ala	
560	565 570 575

FIG.8G.

ATT GAT CCC CAA AGT ACA CAA GGC ACA TCT AAC GTC AAT TTC ACG GCA
 Ile Asp Pro Gln Ser Thr Gln Gly Thr Ser Asn Val Asn Phe Thr Ala
 580 585 590

ACA GTA AAT GGG GCA TTT TAT GGG CCG AAC GCT ACA GAA TTA GGC GGT
 Thr Val Asn Gly Ala Phe Tyr Gly Pro Asn Ala Thr Glu Leu Gly Gly
 595 600 605

TAT TTC ACC TAT AAC GGA AAT CCT ACA GAT AAA AGT TCC TCA ACC GTA
 Tyr Phe Thr Tyr Asn Gly Asn Pro Thr Asp Lys Ser Ser Thr Val
 610 615 620

CCT TCA TCA TCC AAT TCA AAA AAT GCA AGA GCT GCA GTT GTC TTT GGT
 Pro Ser Ser Ser Asn Ser Lys Asn Ala Arg Ala Ala Val Val Phe Gly
 625 630 635

GGC AGA CAA CAA GTA GAA ACA ACC AAA TAATGGAATA CTAAAAAAGA
 Ala Arg Gln Gln Val Glu Thr Thr Lys
 640 645

CTAAAAAAGC TTCTAGAAGC CGAATTC

FIG.9A.

GAATTGGCT TGGATCCAT ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu
1 5 10

TCC TTT TTA CTA AGT GCT TGT AGC GGA GGG GGG TCT TTT GAT GTA GAT
Ser Phe Leu Leu Ser Ala Cys Ser Gly Gly Ser Phe Asp Val Asp
15 20 25

AAC GTC TCT AAT CCA TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT
Asn Val Ser Asn Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr
30 35 40

TCA AGT TCA AGA ACA AAA TCT AAT TTG AAA AAG TTG TCC ATT CCT TCT
Ser Ser Ser Arg Thr Lys Ser Asn Leu Lys Lys Leu Ser Ile Pro Ser
45 50 55

TTA GGG GGA GGG ATG AAG TTA GTG GCT CAG AAT CTT AGT GAT AAG AAC
Leu Gly Gly Gly Met Lys Leu Val Ala Gln Asn Leu Ser Asp Lys Asn
60 65 70 75

AAA CCT AGT CTC TTA AAT GAA GAT GAC TAT ATA TCA TAT TTT TCC TCA
Lys Pro Ser Leu Leu Asn Glu Asp Asp Tyr Ile Ser Tyr Phe Ser Ser
80 85 90

FIG.9B.

CIT TCT ACA ATT CAA GAT GAT GTT AAA GAA AAT AAA CGC CAT ACA	
Leu Ser Thr Ile Gln Asp Asp Val Lys Lys Glu Asn Lys Arg His Thr	95 100 105
AAT CCA GTT GGC TCA ATA GAC GAG CCT AAC GCA ACA AAT CCA CCC GAA	
Asn Pro Val Gly Ser Ile Asp Glu Pro Asn Ala Thr Asn Pro Pro Glu	110 115 120
AAG CAT CAT CGA CAA AGA TAT GTA TAT TCA GCG CTT TAT TAT ATT CCA	
Lys His His Gly Gln Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro	125 130 135
TCG TGG AGT CAT TCC TCA AAT GGC AAG CTT TAT TTA GGT TAC TAT GGA	
Ser Trp Ser His Ser Ser Asn Gly Lys Leu Tyr Leu Gly Tyr Tyr Gly	140 145 150 155
TAT GCG TTT TAT TAT GGT AAT AAA ACT GCA ACA AAC TTG CCA GTA AGC	
Tyr Ala Phe Tyr Tyr Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Ser	160 165 170
GCG ATA GCT AAA TAC AAA GGA ACT TGG GAT TTT ATT ACT GCA ACT AAA	
Gly Ile Ala Lys Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys	175 180 185

FIG.9C.

AAT GGC CAA CGT TAT TCT TTA TTT GGT AGC GCT TTT GGA GCT TAT AAT
Asn Gly Gln Arg Tyr Ser Leu Phe Gly Ser Ala Phe Gly Ala Tyr Asn
190 195 200

AGA CGC AGT GCT ATT TCA GAA GAT ATA GAT AAT TTA GAA AAT AAT CTA
Arg Arg Ser Ala Ile Ser Glu Asp Ile Asp Asn Leu Glu Asn Asn Leu
205 210 215

AAG AAT GGT GCG GGA TTA ACT AGT GAA TTT ACT GTC AAT TTT GGT ACG
Lys Asn Gly Ala Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr
220 225 230 235

AAA AAG CTC ACT GGA AAA CTT TAT TAT AAT GAA AGG GAA ACA AAT CTT
Lys Lys Leu Thr Gly Lys Leu Tyr Tyr Asn Glu Arg Glu Thr Asn Leu
240 245 250

AAT AAA TTA CAA AAG AGA AAA CAT GAA CTC TAT GAT ATA GAT GCC GAT
Asn Lys Leu Gln Lys Arg Lys His Glu Leu Tyr Asp Ile Asp Ala Asp
255 260 265

ATT TAT AGT AAT AGA TTC AGA GGT AAA GTA AAG CCA ACA ACC CAA AAA
Ile Tyr Ser Asn Arg Phe Arg Gly Lys Val Lys Pro Thr Thr Gln Lys
270 275 280

FIG. 9D.

GAT TCT CAA GAA CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT
Asp Ser Gln Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly
285 290 295

TTT TAT GGG CCT AAC GGT GAA GAA TTA GGA GGA AAG TTT TTA GCT GGC
Phe Tyr Gly Pro Asn Gly Glu Glu Leu Gly Gly Lys Phe Leu Ala Gly
300 305 310 315

GAT AAC CGA GTT TTT GGG GTA TTT AGT GGC AAA GAA GAA ACA AAA
Asp Asn Arg Val Phe Gly Val Phe Ser Ala Lys Glu Glu Thr Lys
320 325 330

GAC AAA AAA TTA TCC AGA GAA ACC TTA ATT GAT GGC AAG CTA ATT ACT
Asp Lys Lys Leu Ser Arg Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr
335 340 345

TTT AAA AGA ACT GAT GCA ACA ACC AAT ACA GCA GCC AAT GCA AAA ACC
Phe Lys Arg Thr Asp Ala Thr Thr Asn Thr Ala Ala Asn Ala Lys Thr
350 355 360

GAT GAA AAA AAC TTT ACG ACG AAA GAT ATA CCA AGT TTT GGT GAA GCT
Asp Glu Lys Lys Asn Phe Thr Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala
365 370 375

FIG.9E.

GAT TAC CTT TTA ATT GAT AAT TAC CCT GGT CCT CTT TTC CCT GAA GAA
Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Phe Pro Glu Glu
380 385 390 395

AAT ACT AAT GAT TTC ATA ACT AGT AGG CAC CAT AAG GTA GGA GAT AAA
Asn Thr Asn Asp Phe Ile Thr Ser Arg His Lys Val Gly Asp Lys
400 405 410

ACC TAT AAA GTA GAA GCA TGT TGC AAG AAT CTA AGC TAT GIG AAA TTT
Thr Tyr Lys Val Glu Ala Cys Cys Lys Asn Leu Ser Tyr Val Lys Phe
415 420 425

GGT ATG TAT TAT GAA GAC CCA TTA AAT GGA GAA AAT GGC AAA GAA AAA
Gly Met Tyr Tyr Glu Asp Pro Leu Asn Gly Glu Asn Gly Lys Glu Lys
430 435 440

GAA AAA GAA AAA GAA AAA GAC AAA GAA AAA CAA GCG ACA ACA TCT ATC
Glu Lys Glu Lys Glu Lys Asp Lys Glu Lys Gln Ala Thr Thr Ser Ile
445 450 455

AAG ACT TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT GCC AAG GCC GAC
Lys Thr Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Ala Lys Ala Asp
460 465 470 475

FIG.9F.

ATA CCT GCA ACG GGA AAC GTG AAA TAT CCG GGT AAT TCG TTT GGT TAT
 Ile Pro Ala Thr Gly Asn Val Lys Tyr Arg Gly Asn Trp Phe Gly Tyr
 480 485 490

ATT GGT GAT GAC AAG ACA TCT TAC TCC ACT ACT GGA GAT AAA AAT GCT
 Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Thr Gly Asp Lys Asn Ala
 495 500 505

GTC GCC GAG TTT GAT GTA AAT TTT GCC GAT AAA ACA TTA ACA GGC ACA
 Val Ala Glu Phe Asp Val Asn Phe Ala Asp Lys Thr Leu Thr Gly Thr
 510 515 520

TTA AAA CGA CAC GAT AAT GGA AAT CCC GTA TTT ACA ATT AAT GCA AGC
 Leu Lys Arg His Asp Asn Gly Asn Pro Val Phe Thr Ile Asn Ala Ser
 525 530 535

TTT CAA AGT GGT AAG AAT GAC TTC ACT GGT ACA GCA ACC GCA AAC AAT
 Phe Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Asn Asn
 540 545 550 555

GTA GCG ATT GAT CCC CAA AAT ACA CAA ACC ACA TCT AGA GTC AAT TTC
 Val Ala Ile Asp Pro Gln Asn Thr Gln Thr Ser Arg Val Asn Phe
 560 565 570

FIG. 9G.

ACG GCA ACA GTA AAC GGG GCA TTT TAT GGA CCT AAG GCT ACA GAA TTA
 Thr Ala Thr Val Asn Gly Ala Phe Tyr Gly Pro Lys Ala Thr Glu Leu
 575 580 585

GGC GGT TAT TTC ACT TAT AAC GGA AAC AAT CCT ACA GAT AAA AAT TTC
 Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser
 590 595 600

TCA ACC GTT TCA CCA TCC AAT TCA GCA AAT GCT CGT GCT GCC GTT GTG
 Ser Thr Val Ser Pro Ser Asn Ser Ala Asn Ala Arg Ala Ala Val Val
 605 610 615

TTT GGC GCT AAA AAA CAA GTA GAA ACA ACC AAC AAG TAAAAACAAC
 Phe Gly Ala Lys Lys Gln Val Glu Thr Thr Asn Lys
 620 625 630

CAAGTAATGG AATACTAAAA ATGACTAAAA AAGCTTCTAG AAAGCCGAT TC

FIG.10A.

ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC CTT TTA TTA AGT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Leu Leu Ser
1 5 10 15

GCT TGT AGC GCG GGA GGT GGT TCT TTT GAT GTA GAT GAC GTC TCT AAT
Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn
20 25 30

CCC TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AGT CAA AGA
Pro Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Gln Arg
35 40 45

ACA AAA TCT AAT TTG GAA AAG TTG TCC ATT OCT TCT TTA GGA GGA GCG
Thr Lys Ser Asn Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly
50 55 60

ATG AAA TTG GTG GCT CAG AAT CTG AGT GGT AAT AAA GAA CCT AGT TTC
Met Lys Leu Val Ala Gln Asn Leu Ser Gly Asn Lys Glu Pro Ser Phe
65 70 75 80

TTA AAT GGA AAT GAC TAT ATG ATA TTT TCC TCA CGT TCT ACG ATT AAA
Leu Asn Gly Asn Asp Tyr Met Ile Phe Ser Ser Arg Ser Thr Ile Lys
85 90 95

FIG.10B.

GAT GAT GTT GAA AAT AAC AAT ACA AAC GGG GGG GAC TAT ATT GGC TCA	
Asp Asp Val Glu Asn Asn Thr Asn Gly Gly Asp Tyr Ile Gly Ser	100 105 110
ATA GAC GAG CCT AGT ACA ACA AAT CCA CTC GAA AAG CAT CAT GGA CAA	
Ile Asp Glu Pro Ser Thr Thr Asn Pro Leu Glu Lys His His Gly Gln	115 120 125
AGG TAT GTA TAT TCA GGG CTT TAT TAT ATT CAA TCG TGG AGT CTA AGA	
Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser Leu Arg	130 135 140
GAT TTA CCA AAG AAG TTT TAT TCA GGT TAC TAT GGA TAT GCG TAT TAC	
Asp Leu Pro Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr Ala Tyr Tyr	145 150 155 160
TTT GGC AAG GAA ACA GCC ACT ACA TTA CCT GTA AAT GGC GAA GCA ACG	
Phe Gly Lys Glu Thr Ala Thr Thr Leu Pro Val Asn Gly Glu Ala Thr	165 170 175
TAT AAA GGA ACT TGG GAT TTC ATC ACT GCA ACT AGA AAT GGC AAA AGT	
Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Arg Asn Gly Lys Ser	180 185 190

FIG.10C.

TAT TCT TTG TTA AGT AAT AAC CGA CAA GCT TAT TOC AAA CGT AGT GCA
Tyr Ser Leu Leu Ser Asn Asn Arg Gln Ala Tyr Ser Lys Arg Ser Ala
195 200 205

ATT CCA GAA GAC ATT GAT TTA GAA AAT GAT CCA AAG AAT GGT GAG ACG
Ile Pro Glu Asp Ile Asp Leu Glu Asn Asp Pro Lys Asn Gly Glu Thr
210 215 220

AGA TTA ACT AGT GAA TTT ACT GIG AAT TTT GGT ACG AAA AAG CTC ACA
Arg Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr
225 230 235 240

GGT GGA CTT TAT TAC CAT TTA CGT AAA ACA AAT GCT AAT GAA AAC CAA
Gly Gly Leu Tyr Tyr His Leu Arg Lys Thr Asn Ala Asn Glu Asn Gln
245 250 255

AAT AGA AAA CAT AAA CTC TAC AAT CTA GAA GCT GAT GIG TAT AGC AAC
Asn Arg Lys His Lys Leu Tyr Tyr Asn Leu Glu Ala Asp Val Tyr Ser Asn
260 265 270

CGA TTC AGA GGT AAA GTA AAG CCA ACC AAA GAG TCT TCT GAA GAA CAT
Arg Phe Arg Gly Lys Val Lys Pro Thr Lys Glu Ser Ser Glu Glu His
275 280 285

FIG.10D.

CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT TTT TAT GGG CCT AAT	
Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn	
290	295 300
GCT GAA GAA CTA GGG GGA AAA TTT TTA GCT AGC GAT AAA AAA GTT TTT	
Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Ser Asp Lys Lys Val Phe	
305	310 315 320
GGG GTA TTT AGT GCC AAA GAA GAA CAG CAA GAA ACG GAA AAC AAA AAA	
Gly Val Phe Ser Ala Lys Glu Glu Gln Glu Thr Glu Glu Asn Lys Lys	
325	330 335
TTA CTC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT ACT	
Leu Leu Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr	
340	345 350
AAA AAA ACC AAT GCA ACA ACC GAT GCA ACA ACC AGT ACA ACA ACC AGT	
Lys Lys Thr Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr Thr Ser	
355	360 365
ACA GCA ACC AAT GCA ACA GCC GAT GCA GAA AAC TTT ACG ACA AAA GAT	
Thr Ala Thr Asn Ala Thr Ala Asp Ala Glu Asn Phe Thr Thr Lys Asp	
370	375 380

FIG.10E.

ATA TCA AGT TTT GGT GAA CCT GAT TAT CTT TTA ATT GAT AAT TAC CCT
Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Ile Asp Asn Tyr Pro
385 390 395 400

GTT CCT CTT TTA CCT GAA AAT ACT AAT GAT TTC ATA AGC AGT AAG CAC
Val Pro Leu Leu Pro Glu Asn Thr Asn Asp Phe Ile Ser Ser Lys His
405 410 415

CAT GAG GTA GGA GGT AAA CAC TAT AAA GTG GAA GCA TGT TGC AAG AAT
His Glu Val Gly Gly Lys His Tyr Lys Val Glu Ala Cys Cys Lys Asn
420 425 430

CTA AGC TAT GTG AAA TTT GGT ATA TAT TAT GAG GAT AAT GAG AAG AAC
Leu Ser Tyr Val Lys Phe Gly Ile Tyr Tyr Glu Asp Asn Glu Lys Asn
435 440 445

ACC AAA ATT GAA ACA GAA CAA TAC CAC CAA TTT TTG TTA GGT CTC CGT
Thr Lys Ile Glu Thr Glu Gln Tyr His Gln Phe Leu Leu Gly Leu Arg
450 455 460

ACT CCC AGT TCT CAA ATT CCT GCA ACG GGA AAC GTG AAA TAT CCC GGT
Thr Pro Ser Ser Gln Ile Pro Ala Thr Gly Asn Val Lys Tyr Arg Gly
465 470 475 480

FIG.10F.

AGT TGG TTT GGT TAT ATT GGT GAT GAC AAG ACA TCT TAC TCC ACT ACT
 Ser Trp Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Thr
 485 490 495

GCA GAT AAA AAT GCT CTC GCC GAG TTT GAT GTA AAT TTT ACC GAT AAA
 Gly Asp Lys Asn Ala Leu Ala Glu Phe Asp Val Asn Phe Thr Asp Lys
 500 505 510

AAG CTA ACA GGC GAA TTA AAA CGA GCC GAT AAT CAA AAT ACC GTA TTT
 Lys Leu Thr Gly Glu Leu Lys Arg Ala Asp Asn Gln Asn Thr Val Phe
 515 520 525

AGA ATT AAT GCA GAC TTT AAA AAT AAT GAT AAT GCC TTC AAA GGT ACA
 Arg Ile Asn Ala Asp Phe Lys Asn Asn Asp Asn Ala Phe Lys Gly Thr
 530 535 540

GCA ACC GCA GAA AAT TTT GTA ATA GAT GGT AAC AAT AGT CAA ACT GGA
 Ala Thr Ala Glu Asn Phe Val Ile Asp Gly Asn Asn Ser Gln Thr Gly
 545 550 555 560

AAT ACC CAA ATT AAT ATT AAA ACT GAA GTA AAT GCG GCA TTT TAT GGT
 Asn Thr Gln Ile Asn Ile Lys Thr Glu Val Asn Gly Ala Phe Tyr Gly
 565 570 575

FIG.106.

CCG AAC GCT ACA GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAA AAT
 Pro Asn Ala Thr Glu Leu Gly Tyr Phe Thr Tyr Asn Gly Lys Asn
 580 585 590

CCT ACA GAT AAA AAT TCT GAA AGT TCC TCA ACC GTA CCT TCA CCA CCC
 Pro Thr Asp Lys Asn Ser Glu Ser Ser Thr Val Pro Ser Pro Pro
 595 600 605

AAT TCA CCA AAT GCA AGA GCT GCA GTT GTC TTT GGT GCT AAA AAA CAA
 Asn Ser Pro Asn Ala Arg Ala Ala Val Val Phe Gly Ala Lys Lys Gln
 610 615 620

GTA GAA AAA AAC AAC AAG TAAAAACAAC CAAGTAATGG AATACTAAAA
 Val Glu Lys Asn Asn Lys
 625 630

ATGACTAAAA AAGCTTCTAG AAGCCGAATT C

FIG.11A.

ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT	
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser	15
1 5 10	
GCT TGT AGC GGA GGG GGT TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC	
Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr	30
20 25 30	
CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA ACA	
Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Thr	45
35 40 45	
AAA TCT AAA TTG GAA AAG TTG TCC ATC OCT TCT TTA GGA GGA GGG ATG	
Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Met	60
50 55 60	
AAG TTA GTT GTG CAA AAT TTT GCT GGT GCT AAA GAA CCT AGT TTC TTA	
Lys Leu Val Val Gln Asn Phe Ala Gly Ala Lys Glu Pro Ser Phe Leu	80
65 70 75 80	
AAT GAA AAT GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ATG ATT AAA	
Asn Glu Asn Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Met Ile Lys	95
85 90 95	

FIG.11B.

GAT GAT GTT GAA AAT AAC AAT AAA AAT AAG GAT ACT CCA ATT GGC TCA	
Asp Asp Val Glu Asn Asn Lys Asn Lys Asp Thr Pro Ile Gly Ser	100 105 110
ATA GAC GAG CCT AGA GCA CCA AAT TCA AAC GAA AAT CAT CAA AAT CAT	
Ile Asp Glu Pro Arg Ala Pro Asn Ser Asn Glu Asn His Gln Asn His	115 120 125
CAT GGA CAG CAA TAT GTA TAT TCG GGT CTT TAT TAT ATT CCA TCG TCG	
His Gly Gln Gln Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp	130 135 140
CGT CTA ATA AAT TTA CCA AAT AAG TTT TAT TCA GGT TAC TAT GGA TAT	
Arg Leu Ile Asn Leu Pro Asn Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr	145 150 155 160
GCG TAT TAC TTT GGC AAG CAA ACT GCC ACT ACA TTA CCT GTA AAT GGC	
Ala Tyr Tyr Phe Gly Lys Gln Thr Ala Thr Thr Leu Pro Val Asn Gly	165 170 175
GAA GCA ACG TAT AAA GGA ACT TGG AGC TTC ATC ACC GCA ACT GAA AGA	
Glu Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Thr Glu Arg	180 185 190

FIG.11C.

GGC AAA AAT TAT TCT TTG TTC AAT AAT AGA GGT CAA GCT TAT TCT CGA
Gly Lys Asn Tyr Ser Leu Phe Asn Asn Arg Gly Gln Ala Tyr Ser Arg
195 200 205

CGT AGT GCT ACT CCA GGA GAT ATT GAT TTA GAA AAC GGT GAC GCA GGC
Arg Ser Ala Thr Pro Gly Asp Ile Asp Leu Glu Asn Gly Asp Ala Gly
210 215 220

TTA ACA AGT GAA TTT ACT GTC AAT TTT GGT ACA AAA AAG CTC ACT CGA
Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr Gly
225 230 235 240

GAA CCT TAT TAT AAT GAA AGG GAA ACA AAT CTT AAT CAA TCA AAA GAT
Glu Pro Tyr Tyr Asn Glu Arg Glu Thr Asn Leu Asn Gln Ser Lys Asp
245 250 255

AGA AAA CAT AAA CTC TAC GAT CTA GAA GCT GAT GTG TAT AGC AAC CGA
Arg Lys His Lys Leu Tyr Asp Leu Glu Ala Asp Val Tyr Ser Asn Arg
260 265 270

TTC AGA GGT ACA GTA AAG CCA ACC AAA AAA GAG TCT TCT GAA GAA CAT
Phe Arg Gly Thr Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu His
275 280 285

FIG.11D.

CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAT GGG OCT AAT
Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn
290 295 300

GCT GAA GAA CTA GGG GGA AAA TTT TTA GCT AGC GAT AAA AAA GTT TTT
Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Ser Asp Lys Lys Val Phe
305 310 315 320

GGG GTA TTT AGT GCC AAA GAA ACG GAA GAA AAA CCA AAA TTA CCC AAA
Gly Val Phe Ser Ala Lys Glu Thr Glu Glu Lys Pro Lys Leu Pro Lys
325 330 335

GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT AAA ACA ACC GAT
Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Lys Thr Thr Asp
340 345 350

ACA ACA ACC AAT AAA ACA ACC AGT GCA AAA ACC AAT ACA GAA AAC TTT
Thr Thr Thr Asn Lys Thr Thr Ser Ala Lys Thr Asn Thr Glu Asn Phe
355 360 365

ACG ACA AAA GAT ATA CCA AGT TTT GGT GAA GCT GAT TAT CTT TTA ATT
Thr Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile
370 375 380

FIG.11E.

GAT AAT TAC CCT ATT CCG CTT TTA CCT GAG AGT GGT GAT TTC ATA AGT
 Asp Asn Tyr Pro Ile Pro Leu Leu Pro Glu Ser Gly Asp Phe Ile Ser
 385 390 395 400

AGT AAG CAC CAT GAG GTA GGA GGT AAA CGC TAT AAA GTG GAA GCA TGT
 Ser Lys His Glu Val Gly Gly Lys Arg Tyr Lys Val Glu Ala Cys
 405 410 415

TGC AAG AAT CTA TGC TAT GTG AAA TTT GGT ATG TAT TAT GAG GAT AAA
 Cys Lys Asn Leu Cys Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys
 420 425 430

GAG AAC AAC AAA AAT GAA ACA GAC AAA GAA AAA GAA AAA CAA ACG ACA
 Glu Asn Asn Lys Asn Glu Thr Asp Lys Glu Lys Glu Lys Gln Thr Thr
 435 440 445

ACA TCT ATC AAG ACT TAT TAT CAA TTC TTA TTA GGT CTC CGG ACT CCC
 Thr Ser Ile Lys Thr Tyr Tyr Gln Phe Leu Leu Gly Leu Arg Thr Pro
 450 455 460

AGT TCT GAA ATT CCT AAA ATG GGA AAC GTG ACA TAT CGC GGT AGT TGG
 Ser Ser Glu Ile Pro Lys Met Gly Asn Val Thr Tyr Arg Gly Ser Trp
 465 470 475 480

FIG.11F.

TTT GGT TAT ATT GGT GAT GAC AAG ACA TCT TAC TCC GCT ACA GGA GAT	
Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr Ser Ala Thr Gly Asp	485 490 495
AAA CGA CAA GAT AAA AAT GCT CCC GCC GAG TTT AAT GCT GAT TTT AAC	
Lys Arg Gln Asp Lys Asn Ala Pro Ala Glu Phe Asn Ala Asp Phe Asn	500 505 510
AAT AAA AAG CTA ACA GGC ACA TCA AAA CGA CAC GAT AAT CAA AAT CCC	
Asn Lys Lys Leu Thr Gly Thr Ser Lys Arg His Asp Asn Gln Asn Pro	515 520 525
GIG TTT AAC ATT AAG GCA ACC TTT CAA AAT GGT CGG AAT GAC TTT GAA	
Val Phe Asn Ile Lys Ala Thr Phe Gln Asn Gly Arg Asn Asp Phe Glu	530 535 540
GGT ACA GCA ACC GCA GAA AAT TTT GTA ATA GAT GGT AAA GAT AGT CAA	
Gly Thr Ala Thr Ala Glu Asn Phe Val Ile Asp Gly Lys Asp Ser Gln	545 550 555 560
CGA AAT ACC CCA ATT AAT ATT ACA ACT AAA GTA AAC GGG GCA TTT TAT	
Gly Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr	565 570 575

FIG.11G.

CGA CCT GAT GCT TCT GAA TTA GGC GGT TAT TTC ACC TAT AAC GGA AAA
Gly Pro Asp Ala Ser Glu Leu Gly Tyr Phe Thr Tyr Asn Gly Lys
580 590

GAC ACT ATA ACT AAA AAT ACT GAA AGT TCC TCA ACC GTA CCT TCA CCA
Asp Thr Ile Thr Lys Asn Thr Glu Ser Ser Thr Val Pro Ser Pro
595 600 605

CCC AAT TCA CCA AAT GCA AGA GCT GCA GTT GTG TTT GGA GCT AAA AAA
Pro Asn Ser Pro Asn Ala Arg Ala Val Phe Gly Ala Lys Lys
610 615 620

CAA GTA GAA ACA ACC AAC AAG TAGAAAAAAA CAATAATGG AATACTAAAA
Gln Val Glu Thr Thr Asn Lys
625 630

ATGACTAAAA AAGCTTCTAG AAAGCCGAAT TC

FIG. 12A

TCTAACTTGACATTATTACAAAAGATCAATAATGCGAATTATTATCAATTTGTATGAG...
 TCTAACTTGACATTATTACAAAAGATCAATAATGCGAATTATTATCAATTTGTATGAG...
 TCTAAGTTGACATTATTACAAAAGACAATAATGCGAATTATTATCAATTTGTATGAG...
 TCTAAGTTGACATTATTACAAAAGACAATAATCCGAAATTATTATCAATTTGTATAAG...
 fur-binding site

... 5' GGATCCAT
...
...
... M K S V P L I S G
... TATATAATTCTATGAAATCTGTACCTCTTATCTCTGGT
... TATATAATTCTATGAAATCTGTACCTCTTATCTCTGGT
... TAT-TAATTCTATGAAATCTGTACCTCTTATCTCTCGT
... AATATAATTCTATGAAATCTGTACCTCTTATCTCTCGT

FIG.12B

3' tbp2

GTAGAAACAACCAATAA-----	5' tbp I	
GTAGAAACAACCAATAA-----	M T K K	
GTAGAAACAACCAATAA-----		EAGAN
GTAGAAACAACCAATAA-----		MINNA
GTAGAAACAACCAATAA-----		DL63
GTAGAAACAACCAAGTAAACAACCAAGTAATGGAATACTAAAAATGACTAAAAACCCCTATTTTCGCCTAAGT		PAK

3' IACCTTAIGATTTTACIGATTTTT \CGAAGAICTI 5'

GTAGAAACAACCAATAA-----	M T K K	
GTAGAAACAACCAAGTAAACAACCAAGTAATGGAATACTAAAAATGACTAAAAAA		SB12
GTAGAAACAACCAAGTAAACAACCAAGTAATGGAATACTAAAAATGACTAAAAAA		SB29
GTAGAAACAACCAAGTAAACAACCAAGTAATGGAATACTAAAAATGACTAAAAAA		SB30
GTAGAAACAACCAAGTAAACAACCAAGTAATGGAATACTAAAAATGACTAAAAAA		SB32

FIG.14B.

TQSETVSVSDYTGANRIKPNPMKYESQSWFLRGYHFSE-QHYIGGIFEFTQQKFDIRDMTFPAYLSPTERRDDSSRSFYPMQDHGAYQHIEDGR----	EAGAN
..R.....R...DK.LQ..P...K.Y.....G.....	DL63
S.R.....RS.K.....G.....K.Y.....R.....	PAK
P.....RS.K...RTGP...K.Y...R.....	SB33
DERK...TQ...S..LLA..LE.G...LF.P.W.LDN-R..V.AVL.R...T..T...V...FTSEDYVP-----GSLKGLGKYSGDNKAE.LFVQG	B16B6
DERQ...TR...P..FLAD.LS...R..LF.P.FR.ENKRR...L.H...T..T...V..F.TKAVFDAN.KQAGSLPGNGKYAGNHKY.GLFTNG	M982
DERQ...TR...P..FLAD.LS...R..LF.P.FR.ENKRR...L.H...T..T...V..F.TKAVFDANQKQAGSLPGNGKYAGNHKY.GLFTSG	FA19

-----GVKYASGLYFDEHHRKQRVGIEYIYENKNKAGIIDKAVLSANQQNIILDSYMRHTHCSLYPNPSKNCRPTLDKPYSYRSDRNVYKEKHNMLQL	EAGAN
-----N.....Q.....R.....H.....	DL63
-----N.....R.....H.....	PAK
EGSTLQ.IG.GT.VFY..R.T.N.Y.V..V.H.AD.DTWA.Y.R..YDR.G.D..NRLQQ...HDGSD-...DGN...F.K...MI.E.SR.LF.A	SB33
ENGALV.AE.GT.VFY..T.T.S.Y.L..V.T.AD.DTWA.Y.R..YDR.G.D..NHFQQ...ADGSD- Y..SA...F...K...VI.G.S.RL..A	B16B6
ENNA PV.AE.GT.VFY..T.T.S.Y.L..V.T.AD.DTWA.Y.R..YDR.G.D..NHFQQ...ADG- -Y..SA...F...K...VI.G.S.KL..A	M982
	FA19

NLEKKIQONWLTHQIVFNLGDFDFTSALQHKDYLTRRVIATADSI PRKPGETGKPRNGLSQ-PYLYPKPEPYFAGQDHCNYQSSSYRDCKVRLIKG	EAGAN
.....A.....S..SE.R..A--R.....S-.....T.KAELV.G.L....K....S.....	DL63
.....T...K..SE..AN..--R...YKK..-.....TVG.VV...D.K.N.....	PAK
.....T...NI.SGTVA--R..YEK..-...S.KVG.V.....K....S.....	SB33
VFK.AFD TAKIR.NLSI...Y.R.K.Q.S.S..YLQNAVOAY.L.TP.KPPFP---SKDN-...RVSIGKTTVNTSPI.RFGNNT--Y..TP.N.G.N	B16B6
AFK.SFDTAKIR.NLSV...R.D.N.R.Q..YYQHANRAYS.KTPPKTANP---DK.K-..WVSIGGGNVVTGQI.LFGNNT--Y..TP.S.N..	M982
AFK.SFDTAKIR.NLSV...Y.R.G.N.R.Q..YYQSANRAYS.LKTPPONNGK.TSPNGREKN..WVSIGRGNVVTRQI.LFGNNT--Y..TP.S.N..	FA19

NYFFAARNMALGKYVDLGLGIRYDVSRTKANESTISVGKFKNFWSWNTGIVIKPTEWLDSLRLSTGFRNPFSSEMYGWRVGGKNDDEVVVGKFKPETS RN	EAGAN
.....M.....A.....A.....DTD..I.....	DL63
.....A.....A.....N.S.....	PAK

FIG. 14C.

I.										N. SD.	
G. A. VQD. VR.	RWA. V. A.	YRS. HSEDKSV. T. THR. L.	A. V. L.	FT. M.	T. A.	L. A.	A.	---	ESLKTLDL.	K. F.	B16B6
G. A. V. D. VR.	RWA. V. A. L.	YRS. HSDDGSV. T. THRTL.	A. L.	AD.	T. A.	L. A.	S.	---	VQSKAV. ID.	K. F.	M982
S. A. V. D. VR.	RWA. V. A. L.	YRS. HSDDGSV. T. THRTL.	A. L.	AD.	T. A.	L. A.	S.	---	KIKAV. ID.	K. F.	FA19

QEFLALKGDFG	NIESHFSNAYRNLI	AFAEELSKNG-TGKGN	Y--GYHNAQNAKLVGN	ITAQLDFNGLWKRI	PIYGWYATFAYNQVK	VDQKINAGLAS	EAGAN
.....	T.....	R.....	DL63
.....	N.....	A.....	R.....	PAK
.....	T.....	R.....	SB33
R.A.IVF.....	L.A.Y.N.....	D.....	GY	TRTQNGQTSASGDP	R.....	RIA.I.LGKI.WH.V.GGL.D.L.S.L..RI..	B16B6
K.A.IVF.....	L.A.W.N.....	D.....	VRGY	AQIKNGKEEA	KGDP	A.L..S.RIT.I..LGKI.W..V.DKL.E...S...R.H.R.I.KR.DRTD	M982
K.A.IVF.....	L.A.W.N.....	D.....	VRGY	AQIKDGKEQV	KG	NP	FA19

VSSYLFDAIQPSRYIIIGLYDHPSTNTWGINTMFTQSKAKSQNELCKRALGNNSRD - VKSTRKLTRAWHILDVSGGYMANKNIMRLGIYNLFRYRVVTW	EAGAN
. K N- V.RS.LF L	DL63
. Q N-	PAK
. T VL DGI Y VD SQ . L.GNANAK.AASRR . P.YVT NIK.HLT . A.V . L	SB33
IQ.H VV Q.EGK . V.G.L.Y EIT S L.GNSRNT.A.ARR . P.Y.V TIK.HFT . A.V . L	B16B6
IQ.H VV.S Q.EGK . V.G.L.Y EIT S L.GNSRNT.A.ARR . P.Y.V TVK.HFT . A.V . L.H	M982
	FA19

EAVRQTAQGA	VNQH	VNGSY	TRYA	ASGR	NYTL	LEMKF	*	EAGAN
.....	N.....	*	DL63
.....	*	PAK
.....	*	SB33
N.....	G.....	K.....	V.N.....	P.....	FS.....	*	B16B6
N.....	G.....	G.K.....	V.N.....	P.....	FS.....	*	M982
N.....	A.....	K.....	V.N.....	P.....	FS.....	*	FA19

FIG.15A.

Comparison of TNP2 amino acid sequences

MKSVPLISGGLSACSGG-SFDVDNVSNTPS--SKPRYQDDTS---NQRKKS-NLKKLFIPSLGGGKMLVAQNLRGNREPSFLNEDDYISYFSS	EAGAN
.....T.....G.....D.....PS.....SS.T..-K.E..S.....A.L..FDRNK..L.....S.M-I...	DL63
.....G.....D.....PS.....SS.T..-K.E..S.....FI.AR.....G.M-I...	PAK
.....G.....D.....PS.....SS.T..-K.EN.S.....DRTK..L.....M-I...	SB12
.....L.....G.....D.....PS.....SS.T..-S.....FDRNK..L.....	SB19
.....L.....G.....D.....PS.....S.T..-E.S.....S.....GN..M-I...	SB30
.....L.....G.....D.....PS.....T..-K.E..S.....V..FA.A.....N.....	SB32
MNNPLVNQAAMVLPV.....L..G..L.S.ETVODMH..K.E.EK.Q-PES.QDV.E.SGAAYGFAVKLPRRNAHF.PKYKFKHKP.GSM.WKKLO-R	B16B6
MNNPLVNQAAMVLPV.....L..G..L.S.DT-EAPRPA.K..VS.EKPOA.KD---QG-GYGFAMRLKRRN--WYPGAESEVK...S.WEATGLP	M982
MNNPLVNQAAMVLPV.....L..G..L.S.DT-EAPRPA.K..VP.KKPEARCD---QG-GYGFAMRFRKRRNQHPNSANPKEDEVK.KN..WEATGLP	FA19
MHFKNLPYALFTSL..-V.....KG...LED.RPNKTTGVSKEEYK.VETAKKEQ---GE.ME.A..YV.V---VSSF.NKKVDI---	AP205
MHFKNLPYALFTSL..-V.....KG...LED.RPNQTAKEKATTSYQDEETKKKT.--EE.D..ME.A..YET---I..R..A.KTETGEKRNREV--	AP37

L-----STIEKDVK---DNNKNGADLIGSIDEPTTNPEK---HHGQF-----YVYSGLYYTPSWSLNDSKN-KF-----YLGYYGYAFY	EAGAN
R-----E...---ND.Q..EHP.D..VD.RAP.SN.N---R.....IQ...R.LP.K.....S.....Y.	DL63
.....E..EKVN.....GR.....E..NG.SQNSN---S--E-----ID..RDYKKEEQ.A-----T.....	PAK
.....KA.EK---E..HYTSPV.....K.N---D..R-----I..N..L..N.Y-----Y.S.....Y.	SB12
.....QD..K---E..RHTNPV.....NA.....R-----I..HSSNGKL-----	SB29
.....KD.E---N..T..G.Y.....L.....R-----IQ...R.LPK-----S.....Y.	SB30
.....M.KD.E---N.....KDTF.....RAP.SN.NHQN...Q-----I..R.INLP-----S.....Y.	SB32
GEPNSFSERDE--L..KRG-----SSE--E.KW.DG-----QSRVVGYTNFT..R..YV.LNK-NNI.I..NIV--LFGPDG..Y.K.KEPS	B16B6
TKPKELPKRQK.V...VETDGDSDIYSSPY.TR.NHQNGSAGNVN---QPKNQATGHENFQ.....WF.KHAA.EK.FS.K.I--KSGDDG.IF.H.EKPS	M982
TEPKKLPLKQQ.V.SEVETNGNSKMYTSPY.SQDA.SSH--ANGAN---QPKNEVTDYKKFK....WF.KHAK.EVKNE.GLVSAKRGGDG.IF.H.DKPS	FA19
-----D..VITNGNL.DVPYK.NSSKYNPDI.....KTKDSSLQ..R..YVIDGEH.GSNE-----VY.	AP205
-----VELSED.IT.LYQESVEIIPH.DELNGKTTSDNVYHS---DSKRLDKNRDLK..R..YV.DG.FNEIRNDG.HVFKQGID-----VY.	AP37

FIG.15B.

YGNKTATNLPVNGVAKYKGTWDFITATKNGKRYPLLSNGS--HAYYRRSAIPEDIDLENDKNGDI-GLISEFSADFGTKKLTGQLSYTKRKT-----N EAGAN
F.T.SA..G..T...S...AE..N.E..R.SGGG-Q..S...T...DRKT-----T...TVN.....G.Y.NL.E.DAN-----K DL63
...E.K...K...N...E...S.F..SIG-Q..S...YNLENGDA-----V...K.E...E.Y.NE...SVN-----E PAK
F.KQ...T...KVT...S...AE.....Q..S.FGSAF--G..N...S...NLENNLKNGA-.T...TVN.....K.Y.NE.E.-----H SB12
.....S.I.....Q..S.FGSAF--G..N...S...NLENNLKNGA-.T...TVN.....K.Y.NE.E.-----N SB29
F.KE...T...E.T...R..S.S...NR--Q..SK.....P...ETR-.T...TVN.....G.Y.HL..NAN-----E SB30
F.KQ...T...E.T...S...ER..N.S.FN.RG--Q..S...T.G.....A-.T...TVN.....EPY.NE.E.N-----L SB32
KELP-SEKITYK.TWD.VTDAMEKQRFEG--GSAAGFKSGALSALGVLNRQAEAS--SGHT.F-.MT...EV..SD.TIK.T.YRNN.I.QNNSENKQ B16B6
RQLPASGKVIYK..WHFVTDTKGQDFREIIQPSKKQDRYSGFGSGDSEYYSKNNESTLKDDHEGY-.FT.NLEV..N....K.IRNNASLNNNTNNDK M982
RQLPASEAVIYK..WHFVTDTKGQKFNIDILETSKGQDKYSGFGSGDDEGETSNRT.SNLND.HEGY-.FT.N.KV..NN....K.IRNNKVINTAASDG- FA19
K.SP.KE...QLLT.T.S...TSNANLNNEEGRPNYLN--DD..TKFIGRVLVSG.A.PAKH-KYT.Q.EV..A...M.KJ.-D.E.----- AP205
L.VTPSKE..KGK.IS.....VSNINLEREIDGKDTSGDGKNVSATSITETVNR.HKVGE.L..N-EVKGVAHSSEFAVDFDNKKLTGSLYRNGYINRNK AP37

NQ--PYEKKKLYDIDADIYSNRFRGTVPKTEKD-SEHPFTSEGT-LEGGFYGPNAEELGGKFLATNDRVFGVFSAKETEETKKEA-LSKETLIDGLITFFS EAGAN
S.--NRTH--LE..VH.....K...K.ES.....EGQ.....H.KK.L.....QQ.SENKK.P.....T...K DL63
S.--NTTH--TLE.KV.....K...KTK-.D.....N.EK.....DPQNPENQK..T.....K PAK
I.--NH.....H.....K.N.Q.-K.....EGQ.....G.KK.....G..N.---P.....T... SB12
.NKLQKR.HE.....K...TQKD.Q.....G.....G.....DKK-.R.....K SB29
...--NR.H..NLE..V.....K...KES-.....S.KK.....QQ.EENKK.L.....T... SB30
...SKDR.H...LE..V.....K.ES.....S.KK.....S.KK.....KP.---P.....T... SB32
IK--TTRYTIQATLHGNRFKGAALAD,GATNG--I.DSDS.....KG..A...SN..K.AA..G.QKDKKD.G.NAAGPA.E----- B16B6
HT--TQYYSLDAQ.TGNRFNGTATA.D.KENET-KL-.V.DSSS.S...F..QG...FR.SD.QK.AV.G...TKDKLENG.AA.GS.GAAASGGAAG M982
YT--TEYYSLDATLRGNRF.GKAIA.D..NTGGTKL-.VFDSSS.S...F..QG...FR.SD.GK.AV.G...TKDSTANGNAPAASSG----- FA19
IY--TV---NA..RGNRFTGAATASD.NKG.GE.YNF-.SADSQS.....K...MA...V.N.KSL.A.....- AP205
A.----.VT.R.S.E...AG.....KA.A-..AGD---IFTDSNY.....K...MA...FTNNKSL.A.A..----- AP37

TKKTDAKT---NATTSTAANTTTDTTANTITDEKNFKTEDISSFGADYLLIDKY-----PIPLLPDKNTNDFI EAGAN
.TNAT.NATT--D...T.S.K...T.ATANTE..T.K..P.L.....N.-----V..F.--ESG... DL63
RTDATNTATT--D.K..ATTDA.S-...KK..AE.....P.....GNQ-----E...D... PAK
..T....NATA.....AE.....K.....N.-----V....-ESG... SB12

FIG.15C.

.....T-----A.AK.....T.K.P.....N.....V.F.EE.....SB29
N.T-----D.....S.ATNATA,AE.T.K.....N.....V.....-E.....SB30
 -----KTTD...NK.TSAK.NTE.T.K.P.....N.....-ESG...SB32
 -----VID.YRI.GEEFKKEQIDSGDVKKLLVD.VELS.PSEGNKAA-----FQHEIE-----B16B6
 .S-----SENS--KL..VLD.VEL.LNDKKIKLNDNFNSAAQLVVD.IMIP..PKDSESGNTQADKNGKGTEFTRKFEHTPESDKKDAQAGTQNGAQTASN M982
 PGAATMPSET--RL..VLD.VEL.PDGKEIKLNDNFNSATRLVVD.IMIP..PT--ESGNGQADKNGKGTDFTYETTVTPESDKKDKTKAQTGAGGMQTASG FA19
 -----HNGSNVN.VRIIDASKI.LT..SISELNN..D.SV.I.....-GKKIKLAGSG.T AP205
 -----SENG--ET..E-----RIIDA.KI.LTQ.NAKELNN..D.SV.I.....-GQKI.LAGVN.K AP37

SSKHHTVGNKR--YKVEACCSNLSYVKFGMYEDPLKEKETETETETETEKDEKEKEKDKKEKQTAATNTYYQFLLGHRTPKDDIPK--TGSACYHGSWFG EAGAN
K.T--Q.....A.P.--E.K.K.KD.....ATTSIK.....L..SSE.....-E.....N...DL63
G.T--K.....K.....KDKDN.NETDKEKGKPT.TTSI.....L.....E.....-E.....N...PAK
K.T--Q.K.....V.P.E.....--KE.E...ATNLS.....L..SSE.....-G.....L....SB12
 T.R..K..D.T--K.....K.....--NG.NG.....E.....ATTSIK.....A.A...A--..NV..R.N...SB29
E.G.H--K.....K.....I.....--N..N.KIE.EQ.H...L..SSQ..A--..NV..R.....SB30
E.G.--K.C.....K.....--KENNKN.T.E.....TTSIK.....L..SSE.....-M.NVT.R.....SB32
 ---QNGVKAT---V.....D.MS..KLSKEN---DDM..Q.V...VS.VAARTEAN...R.T.Y..B16B6
 TAGDTNGKT.T--E.V.....N.L.Y..LTRKNS.---SAMQAGNSSQADAKTEQVEQSM..Q.E..DEKE...--TDQNVV.R...Y..M982
 TAGVNGGQVGTKT...QV.....N.L.Y..LLTREN-----NNSVMQAVKNSS.AD.K.KQIE.SMFLQGERT.ENKIPQEQGIV.L.F.Y..FA19
 NKHTIEING.T--MVAV.....E.M...QLW-----QQAEGGKPENNSL..Q.E..AT.KM...--G.NY..I.T.D-AP205
 N..TVEING.T--MVAV.....E.M...QLW-----Q.EGKQQVKDNSL..Q.E..AT.KM.A--G.NY..V.T.D-AP37

YITDGKTSYSPSGDKKRDKNAEAFNVDFAEKKLTGELKRHDGTG-NPVFSIEANFNSSNAFTGTATATN--FVIDGKNSQNKNTPINITTKVNGAFYCPKA EAGAN
 ...S.E...A...E.S.....N.....T.....Q-...K.N.T.QSGK.D.....KD--LA....T.GTSKVNFTA.-...DL63
 ...S.E...A...E.S.....D.S.N.T.....N.-T.K.N.EL.G.-D.....N..TS.AK.....PAK
 .LS.S.....EN.L.....N.VD.T.KGQ.I..NQ-.T..T.D.T.KGCK.N.....N.--VA..POSTQGTSNVNFTA.-...N..SB12
 .G.D.....TT.....D.N..D.T...T.....N.....T.N.S.QSGK.D.....N.--VA..PQ.T.TTSRVNFTA.-...SB29
 .G.D.....TT.....L...D.N.TD.....A.NQ-.T..R.N.D.K.ND...K.....E.--N..TG..Q...K.E.....N..SB30
 .G.D.....AT...RQ.....P...A.NN.....TS.....NQ-...N.K.T.Q.GR.D.E.....E.--D..G-...SB32

FIG. 15D.

..AN.-..W.GEASNQEGG.-R...D...ST..IS.T.TAK.RT-S.A.T.T.MIKD--.G.S.V.KTGENG.AL.PQ.TG.SHYTHI-EAT.S.G...KN. B16B6
H.AN.-..W.GNASD.EGG.-R...T.N..D..I..K.TAENRQ-AQT.T.GMIQG--.G.E..KTAESG.DL.Q..TTRTPKAYITDA..K.G..... M982
R.AN.-..W.GKASNAT.G.-R.K.T.N.DR.EI..T.TAENRS-EAT.T.D.MIEG--.G.K..KTG.DG.AP.QN..TVTHKVHIANAE.Q.G...N. FA19
AQVSKENNWVATA.DD.KSGYRT..D...GN.N.Ş.K.LFDKN.V....TVD.KIDG--.G..K.KTSDEG.AL.SGS.RYE.VKF.DVA-.S.G...T. AP205
ALVSKG.NWIAEA.NN.ESGYRT..D.N.SD..VN.K.-FDKG.V....TVD.TI.G--.G.I.S.KTSDSG.AL.AGS..HG.AVFSDI-...G...T. AP37

SELGGYFTYNGN - STATNSESSSTVSSSSNKNARA	VVFGAR - QQVETT - K*	EAGAN
T.....	-----NPTDKN.....EK.....KK.....-	DL63
.....KNP.....P.PP.P.S.....KK-.....N.*	PAK
T.....	----PTDK.....P.....-.....-	SB12
T.....	----NPTDKN.....P.-.A.....KK-.....N.*	SB29
T.....	KNP.DK.....P.PP.P.....KK-.....KNN.*	SB30
.....	KDTITK.T.....P.PP.P.....KK-.....N.*	SB32
I.M.S.SFP..APEGKQE-----	-----K.S.....KR.LVQ*	B16B6
E...W.A.P.DKQ.EKAT-----	AT.DGNSASS.T.....KR.PVQ*	M982
E...W.A.P.EQ.KNA-----	E.GNGNSASS.T.....KR.KLVK*	FA19
A...Q.HHKSENGSVGA-----	-----K-...KK*	AP205
G...Q.HHKSDNGSVGA-----	-----K-R.I.K*	AP37

FIG.16A'.

FIG.16A'.

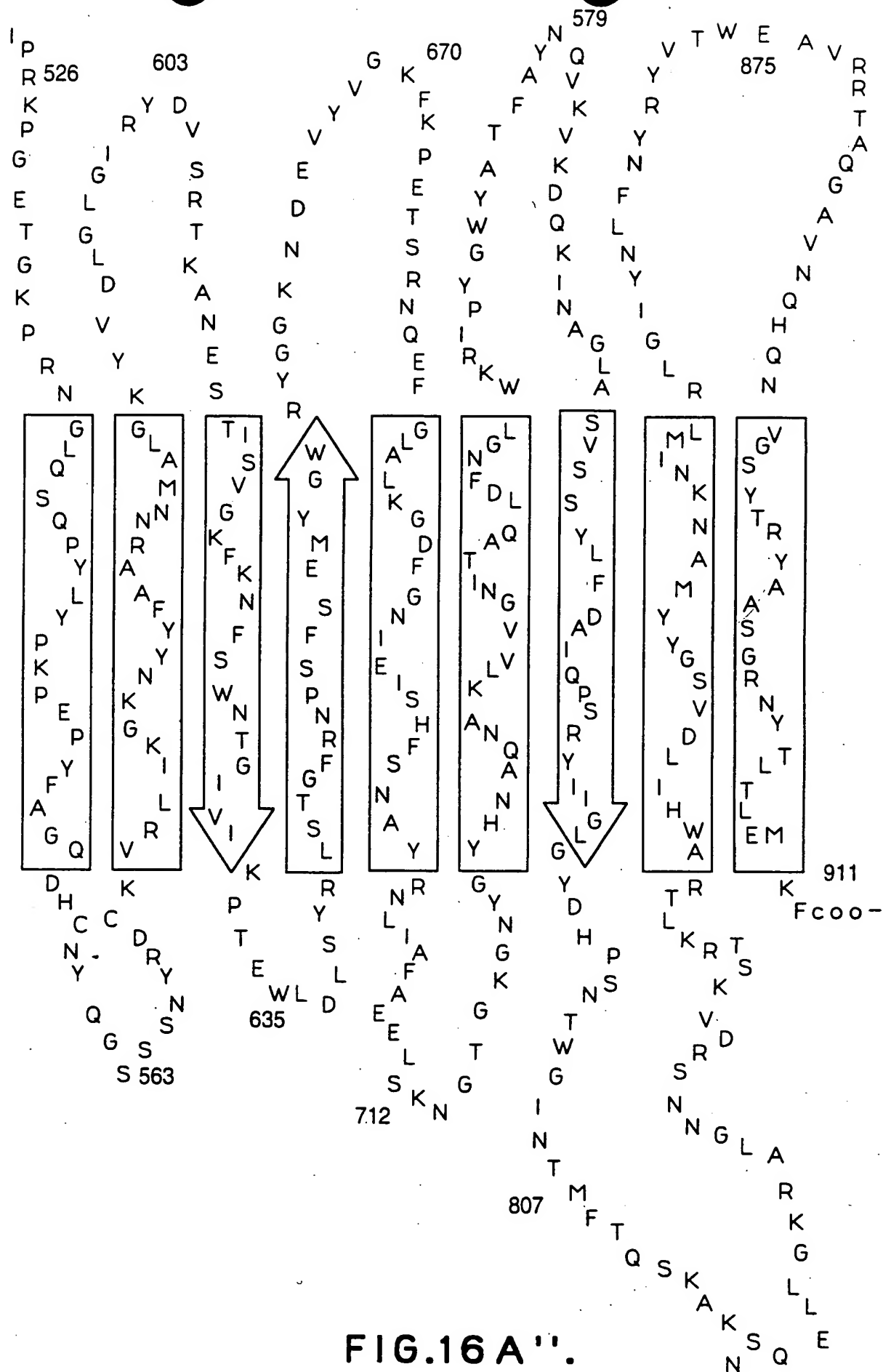


FIG.16A''.

20470-44E4007

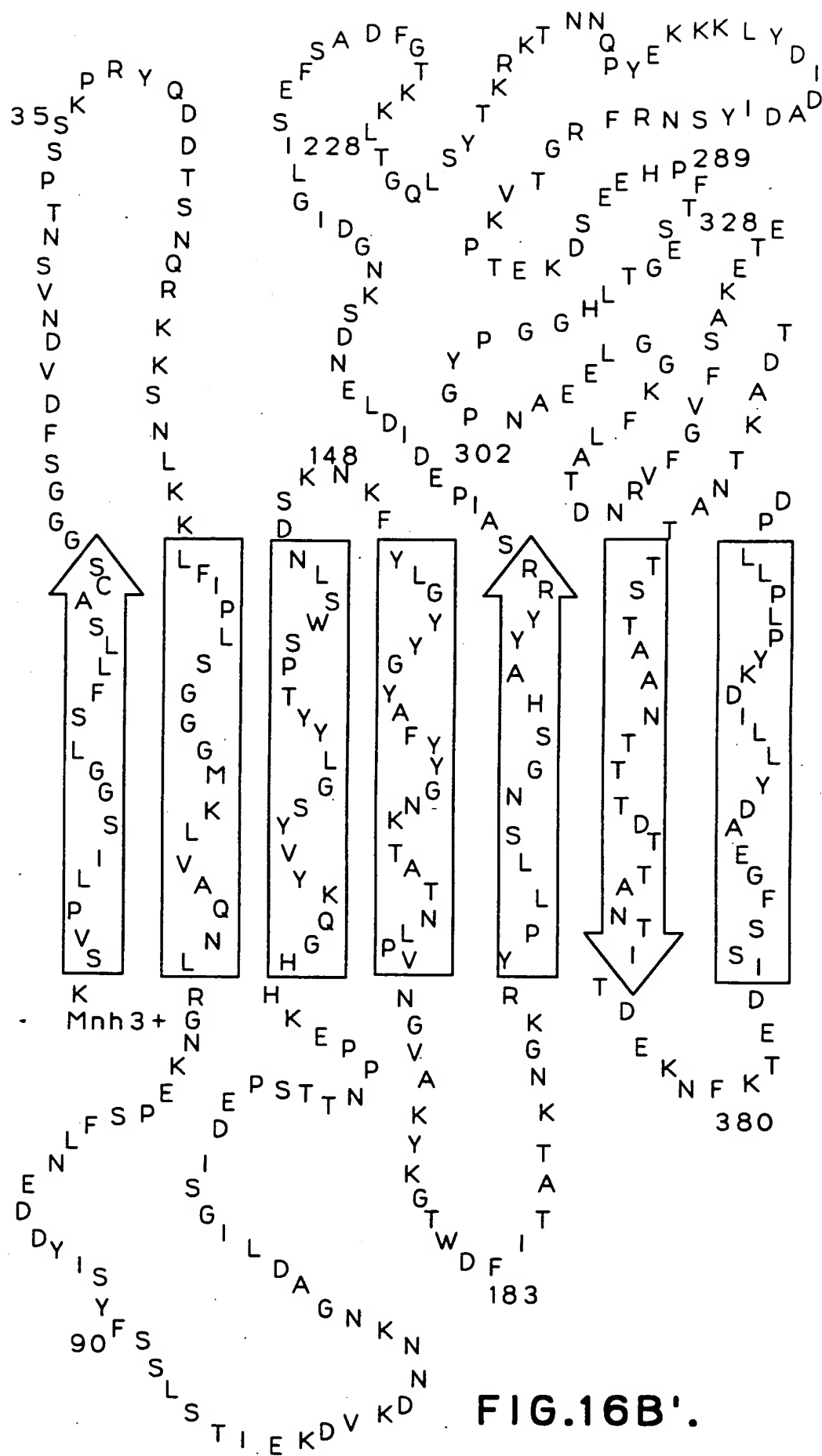


FIG.16B'.

FIG.16B''.

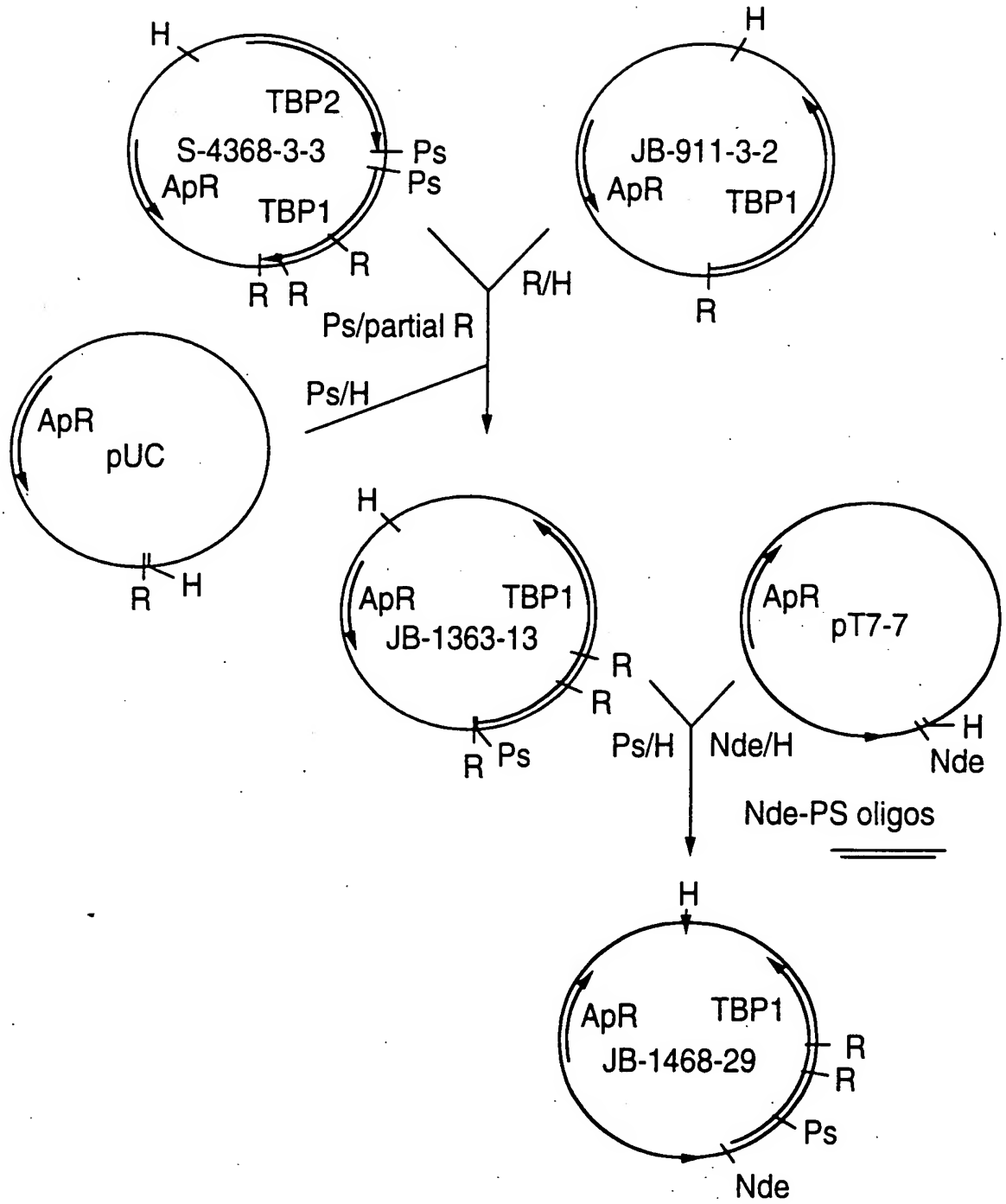


FIG.17.

204770-442400

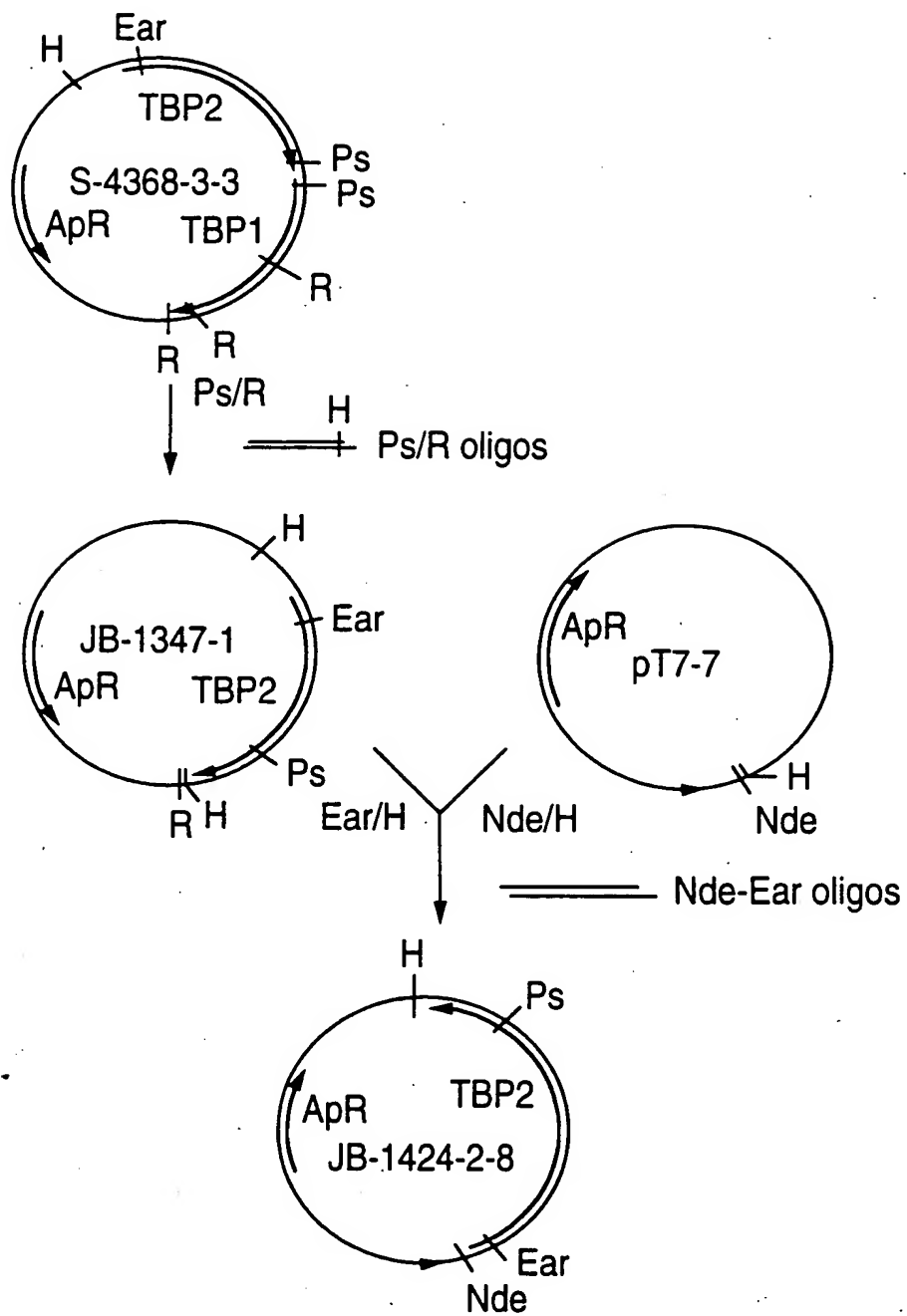


FIG.18

FIG.19. Oligonucleotides to express TBP2 with no signal sequence.

Nde I

Ear I

TATGTGTTCTGGTGGTGTCTTTCGACGTTGACAAACGTTTCTAACACTCCCTCTTCT
ACACAAGACCACCAAGAAAGCTGCAACTGTTGCAAGATTGTGAGGGAGAGATTT

ATG start codon is underlined

TGT cysteine of mature protein is double underlined

FIG.20A.

Sequence of oligonucleotide pairs (A, B, C and D) for constructing TBP1 and TBP2 expression plasmids

Oligonucleotide pair A (Seq. ID 86 and 87) to join the T7 promoter and Egan TBP1 gene

Nde I

TATGAAACTCAAAGTATAAAAGATACAAAAGAAGCTATATCATCTGAAGT...
ACCTTGAGTTTCATATTTTCTATGTTTCTTCGATATAGTACTTCA...

Pst I

...GGACACTCAAAGTACAGAAGATTTCAGAAATTAGAAACTATCTCAGTCACTGCA
...CCTGTGAGTTTCATGTCTTCTAAGTCTTAATCTTTGATAGAGTCAGTG

Oligonucleotide pair B (Seq. ID 88 and 89) to join the T7 promoter and Egan TBP2 genes through the *E. coli* lpp leader

Nde I

TATGAAAGCTACTAAACTGGTTCTGGGTGCTGTTATCCTGGGTCCACTCTG...
ACTTTCGATGATTGACCAAGACCCACGACAATAGGACCCAAAGGTGAGAC...

Ear I

...CTGGCTGGTTGTAGCGGAGGTGGTTGTTTGTATGATAGATAACGTCTCTAATACCCCTCTTCT
...GACCCACCAACATCGCCTCCACCAACAAACTACATCTATTGCAGAGATTATGGGGGAGAAGATT

FIG. 20B.

Oligonucleotide pair C (Seq. ID 90 and 91) to join the T7 promoter and Egan TBP2 genes through the *E. coli* rlp B leader

Nde I

TATGCGATATCTGGCAACATTTGTTATCTCTGCGGTGTTAATCACCGCTG...
ACGCTATAGACCGTTGTAACAACAATAGAGACCGCCACAATTAGTGGGAC...

Ear I

...GTTGTAGCGAGGTGTTCTTTTGATGTAGATAACGTCTCTAATACCCCTCTTCT
...CAACATCGCCTCCACCAAGAAACTACATCTATTGCAGAGATTATGGGGGAGAAGATT

Oligonucleotide pair D (Seq. ID 92 and 93) to join the T7 promoter and Egan TBP2 genes through the *E. coli* pal leader

Nde I

TATGCAACTGAACAAGTCTGAAAGGCTGATGTTGCTCTGCCTGTTATGGCAA...
ACGTTGACTTGTTTACGACTTCCCGACTACTAACGAGACGGACAATACCGTT...

Ear I

...TTGCTGGTTGTAGCGAGGTGTTCTTTTGATGTAGATAACGTCTCTAATACCCCTCTTCT
...AACGACCAACATCGCCTCCTACCAAGAAACTACATCTATTGCAGAGATTATGGGGGAGAAGATT

ATG start codons are underlined

TGT coding for Cys of lipoproteins are double underlined

TGT may be replaced by TCC coding for Ser to secrete non-lipoprotein

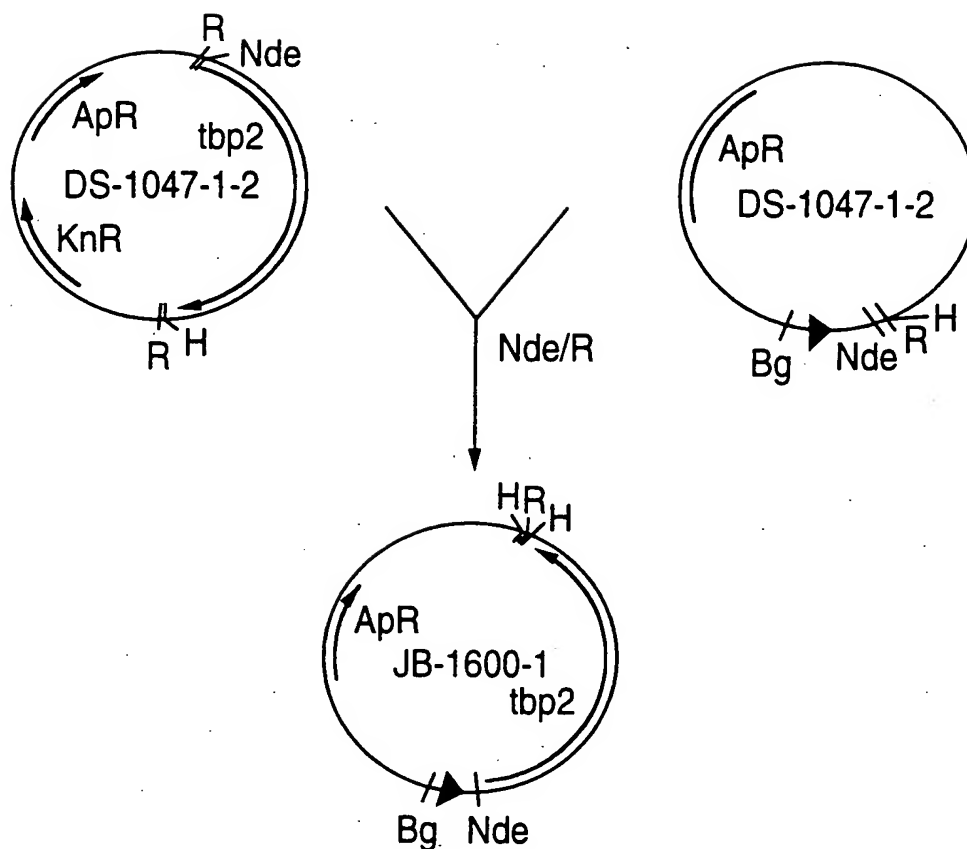


FIG.21.

10043344-01.402

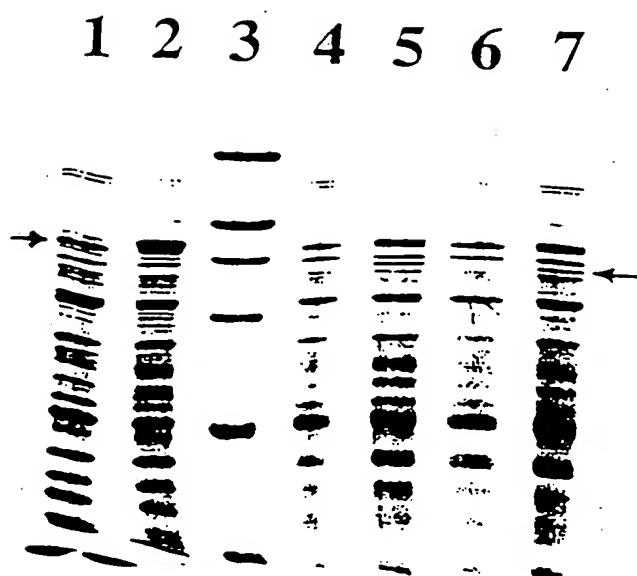


FIG.22.

PURIFICATION OF rTBP1/ rTBP2 FROM *E. COLI*

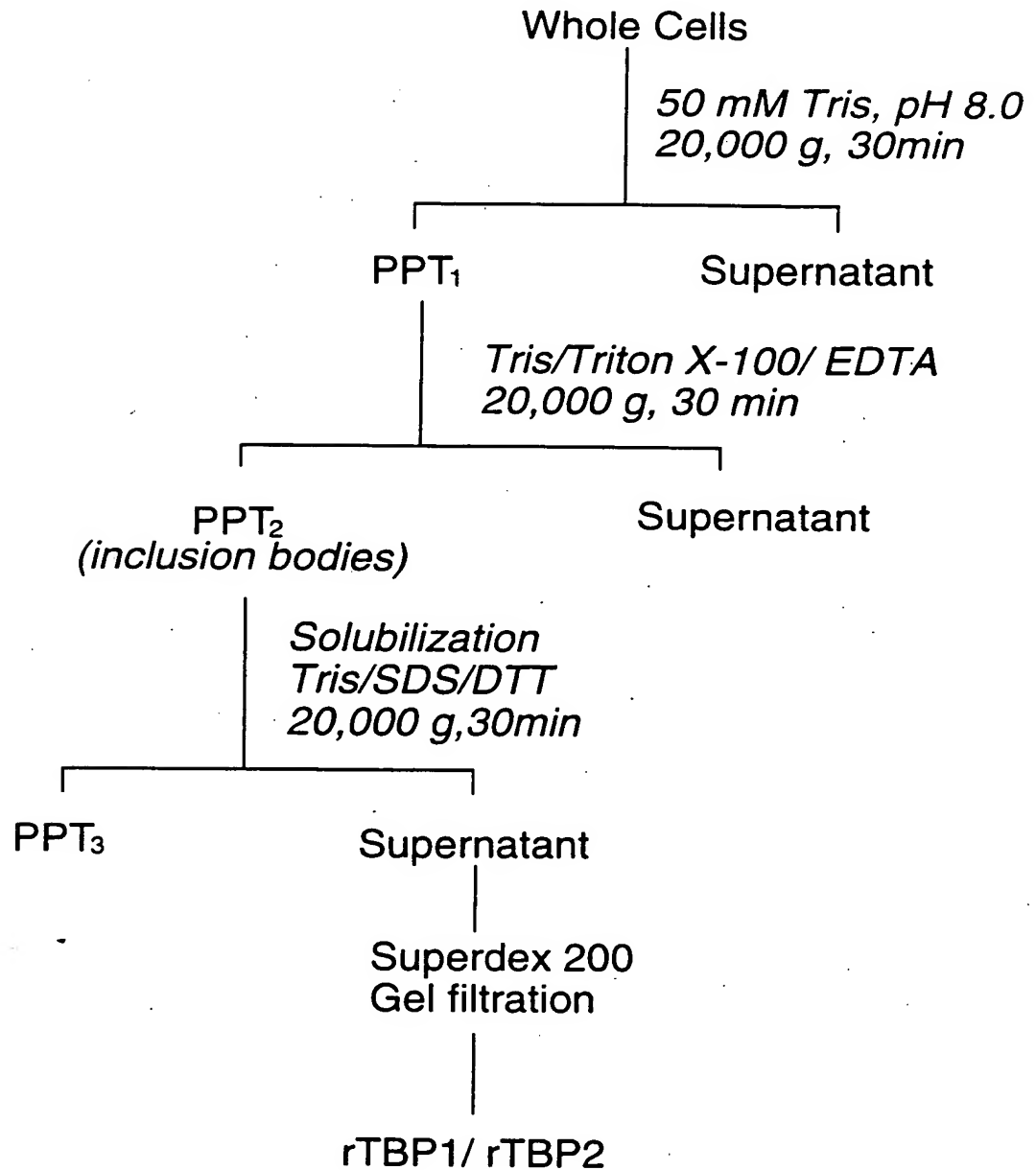


FIG.23.

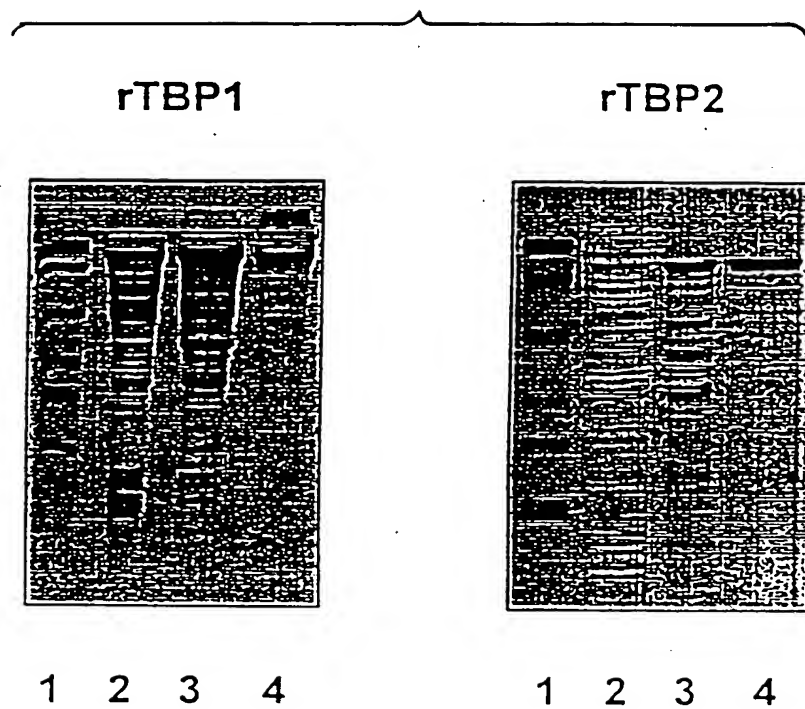


FIG 24

Kinetics of Antibody Response to TBP1/TBP2 in Mice

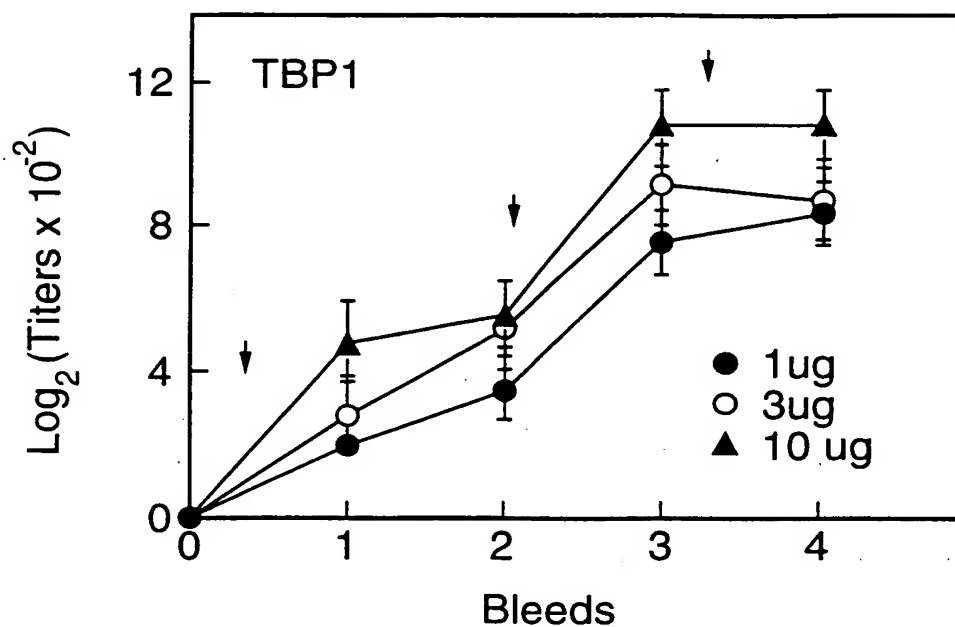


FIG.25A.

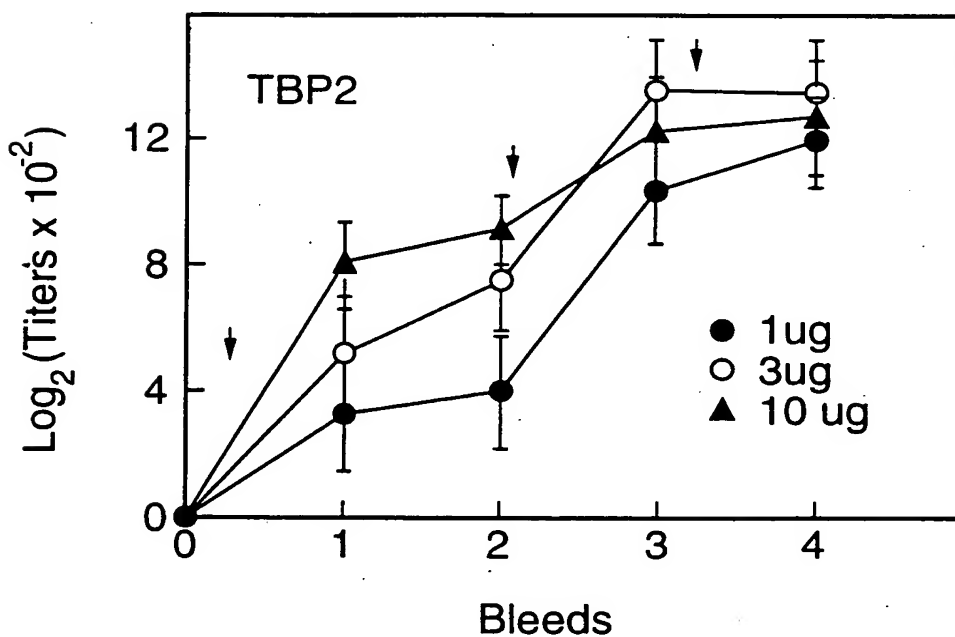
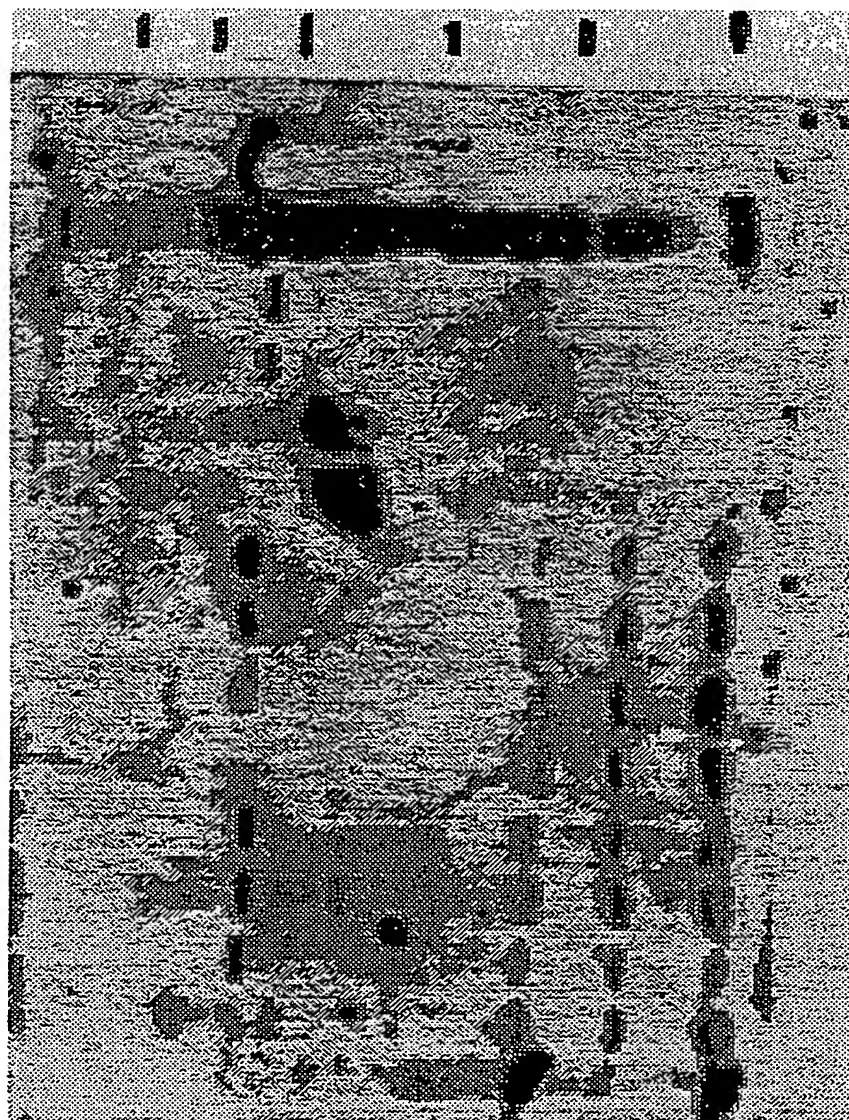


FIG.25B.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15



202
133
71
41
31
18

FIG.26.

20470-44E400F

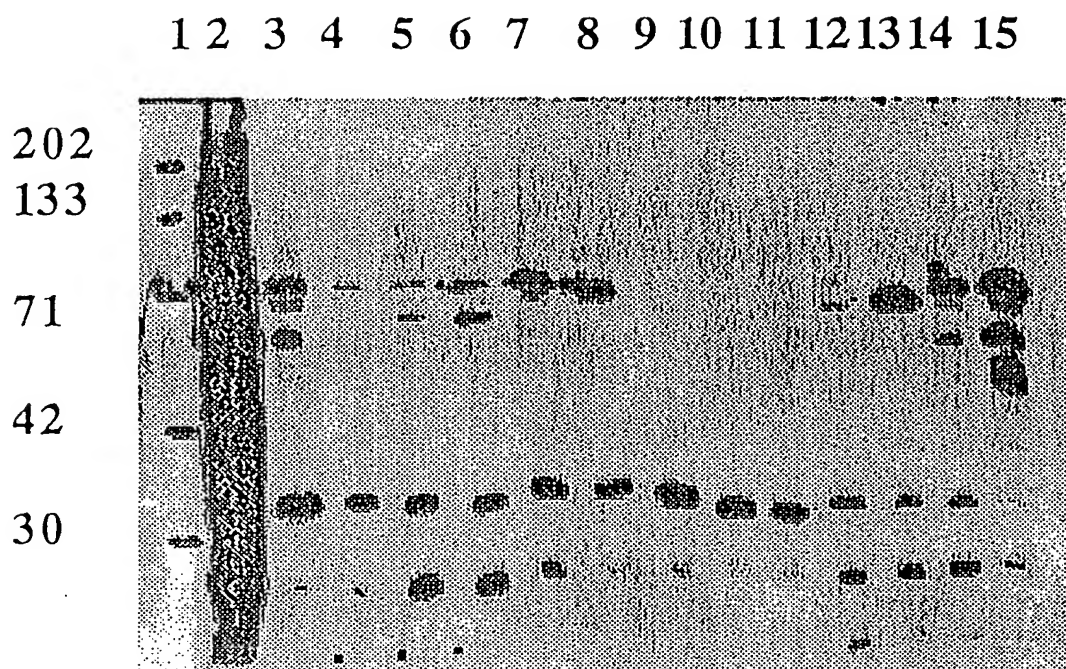
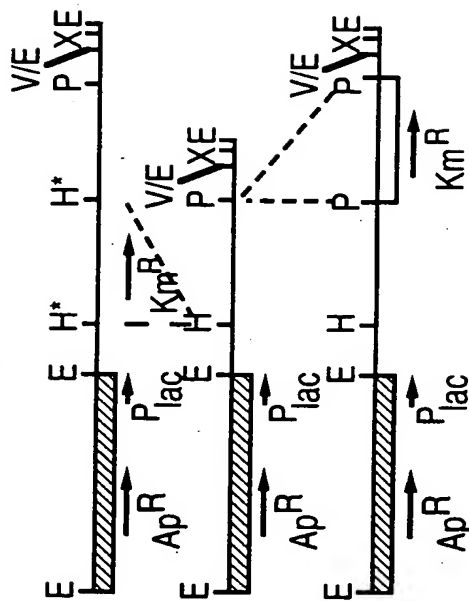
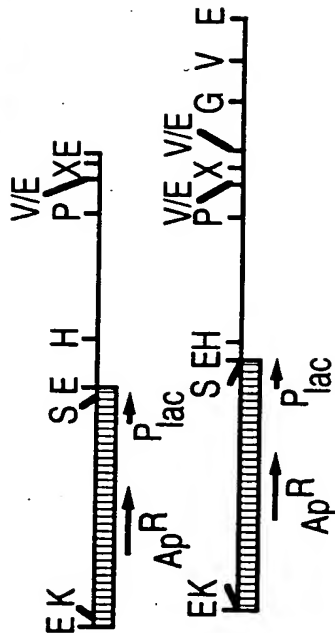
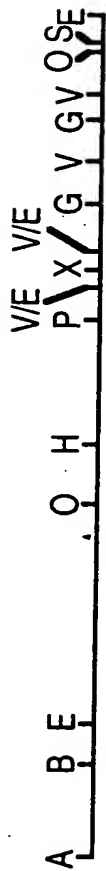


FIG. 27.

Construction of plasmids pUHIT1KFH and pUHIT1KFP

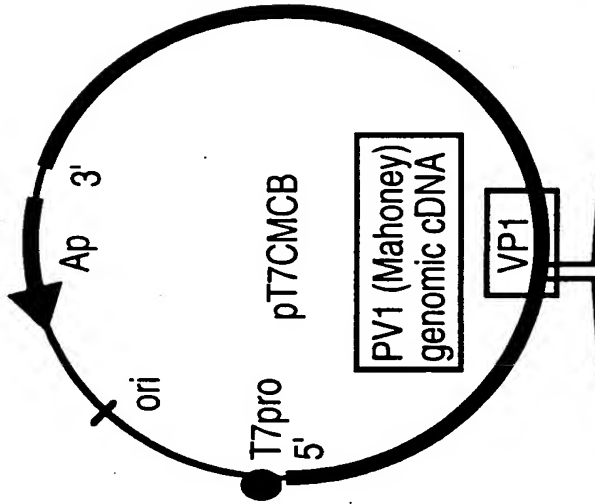
DL63 Wild Type
Chromosomal Map



- chromosomal DNA
- ▨ pBluescript SK+
- ▤ pUC4K
- pUC4K Km^R cassette

1kb

FIG.28.



Sal I

Hind III

nt 2753 GTC GAC AAC CCA GCT TCC ACC ACC AAT AAG GAC AAG CTT 2791
CAG CTG GGT CGA AGG TGG TGG TTA TTC CTG TTC GA A

aa1094 V D N P A S T T N K D K L 1102

Clone	Sequence encoded	SEQ.	Viabile virus
		ID NO:	recovered/ strain designation

pT7XLD	NPASTTNKD	132	Yes/PV1-XLD
pT7TBP2A	NPASTTSLEGGFYGPKD	133	Yes/PV1TBP2A
pT7TBP2B	NPASTTSLEGGFYGKD	134	Yes/PV1TBP2B
pT7TBP2C	NPASTTLEGGFYGPKD	135	Yes/PV1TBP2C
pT7TBP2D	NPASTTLEGGFYGKD	136	Yes/PV1TBP2B

FIG.29.

FIG. 30.

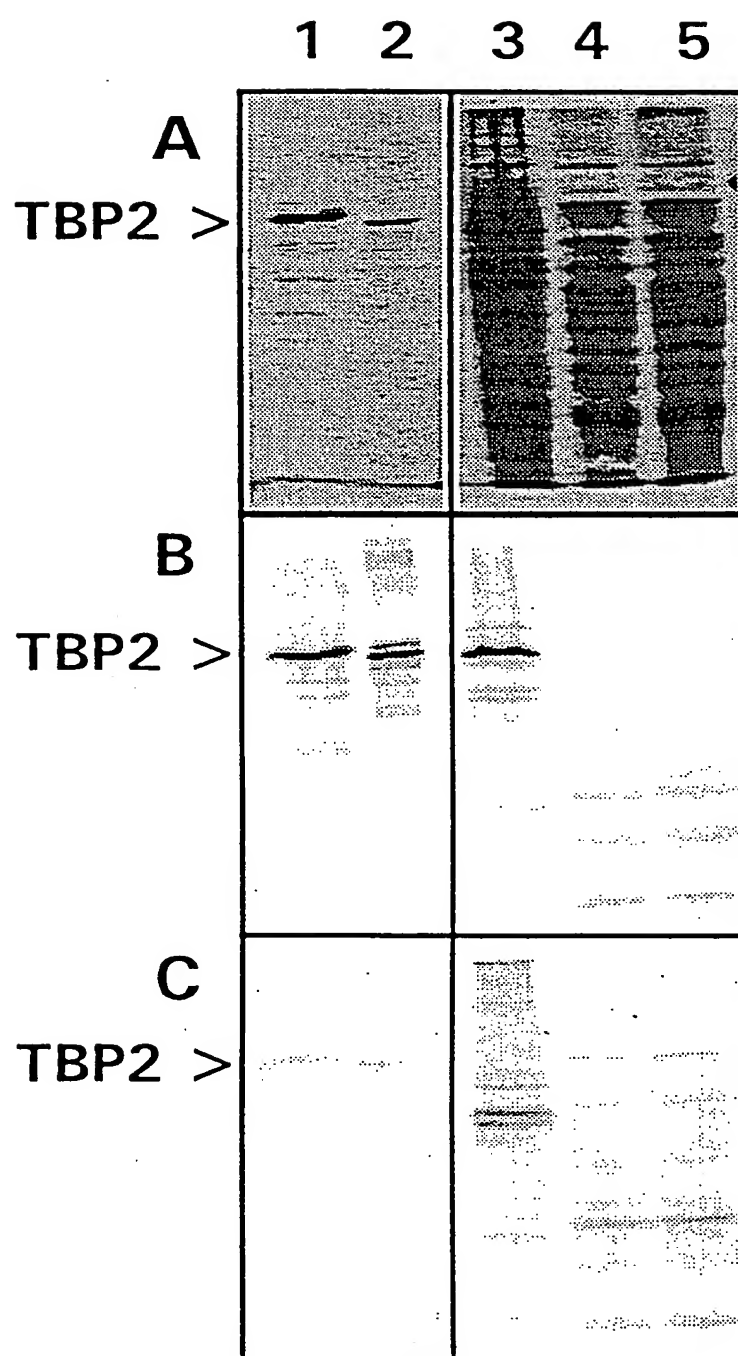


FIG.31A

Eagan Tbp2

MKSVPLISGGLSFLLSACSGGGSFVDNVSNTPSSKPRYQDDTSNQKKKS

Signal Sequence

DS-1466-1-18



NLKKLFIPSLGGMKLVAQNLRGNKEPSFLNEDDYISYFSSLSTIEKDVK

DS-1466-4-3



DNNKNGADLIGSIDEPTTNPPEKHHGQKYVYSGLYYTPSWSLNDSKNKF

YLGYYGYAFYYGNKTA TNLPVNGVAKYKGTWDFITATKNGKRYPLLSNGS

HAYYRRSAIPEDIDLENDSKNGDIGLISEFSADFGTKKLTGQLSYTKRKT

DS-1466-5-1



NNQPYEKKKLYDIDADIYSNRFRGTVKPT EKDSEEH PFTSEGTLEGGFYG

DS-1466-4-1



PNAEELGGKFLATDNRVFGVFSAKETEETKKEALSKETLIDGKLITFSTK

FIG.31B

DS-1457-3-1



KTDAKTNATSTAAANTTTDTTANTITDEKNFKTEDISSFGEADYLLIDKY

DS-1466-1-4 DS-1466-7-9 DS-1466-3-1 DS-1466-3-4



PIPLLPDKNTNDFISSKHHTVGNKRYKVEACCSNLSYVKFGMYEDPLKE

DS-1466-2-6



KETETETETEKDKEKEKDKEKQTAATTNTYYQFLLGHRTPKDDIPK

DS-1461-1-1 DS-1466-1-14

DS-1466-1-1



TGSAKYHGSWFGYITDGKTSYSPSGDKKRDKNVAEFNVDFAEKKLTGEL

KRHDTCNPVFSIEANFNSSNAFTGTATATNFVDGKNSQNKNTPINITT

DS-1461-8-1



KVNGAFYGPKASELGGYFTYNGNSTATNSESSSTVSSSSNSKNARAAVVF

GARQQVETTK*

SDS-PAGE

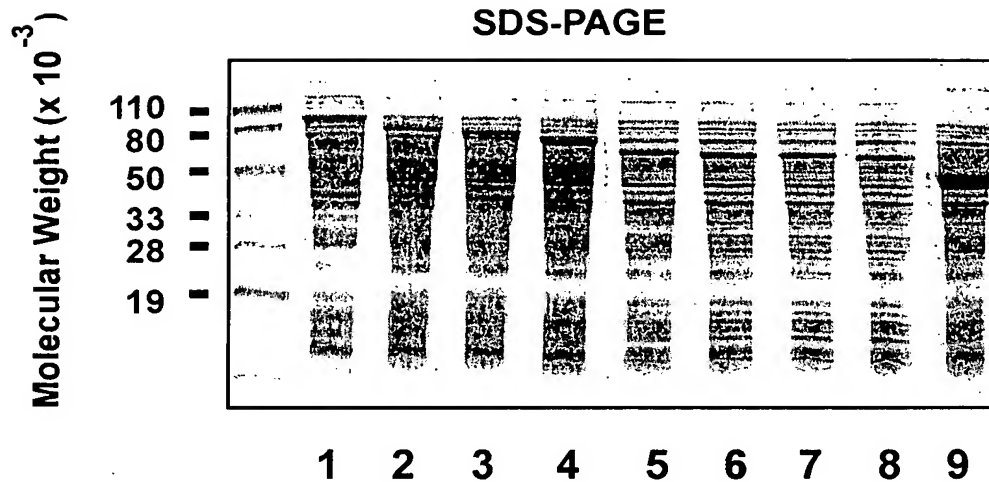


FIG 32 A.

HTf- Binding

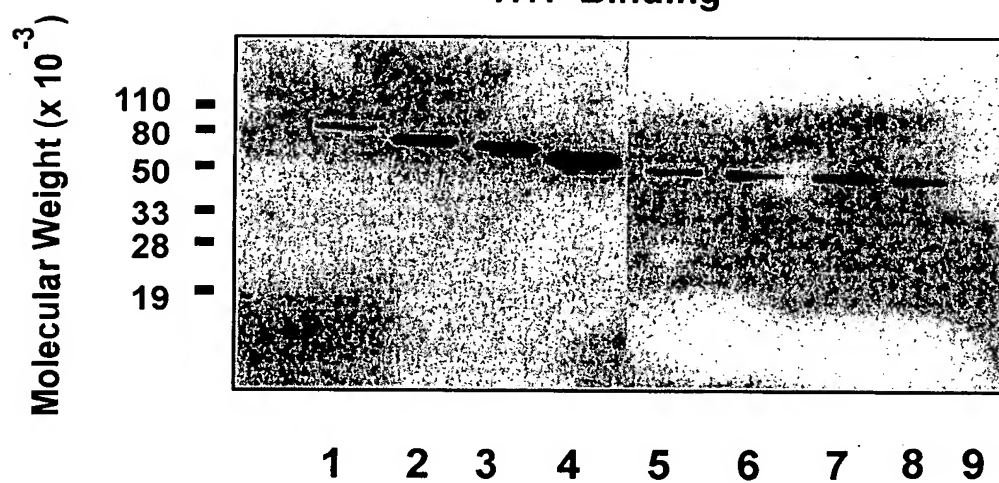


FIG 32 B.